

```

1 ATGTCCAGCG CTCGGACCCC CCTACCCACG CTGAACGAGA GGGACACGGA
51 GCAGCCCACC TTGGGACACC TTGACTCCAA GCCCAGCAGT AAGTCCAACA
101 TGATTCGGGG CCGCAACTCA GCCACCTCTG CTGATGAGCA GCCCCACATT
151 GGAAACTACC GGCTCCTCAA GACCATTGGC AAGGGTAATT TTGCCAAGGT
201 GAAGTTGGCC CGACACATCC TGAAGGTTT GAATCATCCC AACATAGTTA AATTATTTGA
251 TTGACAAGAC TCAACTGAAC TCCTCCAGCC TCCAGAACT ATTCCGCGAA
301 GTAAGAATAA TGAAGGTTTT GAATCATCCC AACATAGTTA AATTATTTGA
351 AGTGATTGAG ACTGAGAAAA CGCTCTACCT TGTCTAGGAG TACGCTAGTG
401 GCGGAGAGGT ATTTGATTAC CTAGTGGCTC ATGGCAGGAT GAAAGAAAAA
451 GAGGCTCGAG CCAAATTCCG CCAGGTAGTG TCTGCTGTGC AGTACTGTCA
501 CCAGAAGTTT ATTTGTCATA GAGACTTAAA GGCAGAAAAC CTGCTCTTGG
551 ATGCTGATAT GAACATCAAG ATTGCAGACT TTGGCTTCAG CAATGAATTC
601 ACCTTTGGGA ACAAGCTGGA CACCTTCTGT GGCAGTCCCC CTTATGCTGC
651 CCCAGAACTC TTCCAGGGCA AAAAATATGA TGGACCCGAG GTGGATGTGT
701 GGAGCCTAGG AGTTATCCTC TATACACTGG TCAGCGGATC CCTGCCTTTT
751 GATGGACAGA ACCTCAAGGA GCTGCGGGAA CGGGTACTGA GGGGAAAATA
801 CCGTATTCCA TTCTACATGT CCACGGACTG TGAAAACCTG CTTAAGAAAT
851 TTCTCATTCT TAATCCCAGC AAGAGAGGCA CTTTAGAGCA AATCATGAAA
901 GATCGATGGA TGAATGTGGG TCACGAAGAT GATGAACTAA AGCCTTACGT
951 GGAGCCACTC CCTGACTACA AGGACCCCCG GCGGACAGAG CTGATGGTGT
1001 CCATGGGTTA TACACGGGAA GAGATCCAGG ACTCGCTGGT GGGCCAGAGA
1051 TACAACGAGG TGATGGCCAC CTATCTGCTC CTGGGCTACA AGAGCTCCGA
1101 GCTGGAAGGC GACACCATCA CCCTGAAACC CCGGCCTTCA GCTGATCTGA
1151 CCAATAGCAG CGCCCCATCC CCATCCCACA AGGTACAGCG CAGCGTGTGC
1201 GCCAATCCCA AGCAGCGGCG CTTACAGCGAC CAGGCTGGTC CTGCCATTCC
1251 CACCTCTAAT TCTTACTCTA AGAAGACTCA GAGTAACAAC GCAGAAAATA
1301 AGCGGCCTGA GGAGGACCGG GAGTCAGGGC GGAAAGCCAG CAGCACAGCC
1351 AAGGTGCCTG CCAGCCCCCT GCCCGGTCTG GAGAGGAAGA AGACCACCCC
1401 AACCCCTCC ACGAACAGCG TCCTCTCCAC CAGCACAAT CGAAGCAGGA
1451 ATTCCCCACT TTTGGAGCGG GCCAGCCTCG GCCAGGCCTC CATCCAGAAT
1501 GGCAAAGACA GCACAGCCCC CCAGCGTGTC CCTGTTGCCT CCCCATCCGC
1551 CCACAACATC AGCAGCAGTG GTGGAGCCCC AGACCGAACT AACTTCCCCC
1601 GGGGTGTGTC CAGCCGAAGC ACCTTCCATG CTGGGCAGCT CCGACAGGTG
1651 CGGGACCAGC AGAATTTGCC CTACGGTGTG ACCCCAGCCT CTCCCTCTGG
1701 CCACAGCCAG GGCCGGCGGG GGGCCTCTGG GAGCATCTTC AGCAAGTTCA
1751 CCTCCAAGTT TGTACGCAGG AACCTGAATG AACCTGAAAG CAAAGACCGA
1801 GTGGAGACGC TCAGACCTCA CGTGGTGGGC AGTGGCGGCA ACGACAAAGA
1851 AAAGGAAGAA TTTCGGGAGG CCAAGCCCCG CTCCCTCCGC TTCACGTGGA
1901 GTATGAAGAC CACGAGCTCC ATGGAGCCCA ACGAGATGAT GCGGGAGATC
1951 CGCAAGGTGC TGGACGCGAA CAGCTGCCAG AGCGAGCTGC ATGAGAAGTA
2001 CATGCTGCTG TGCATGCACG GCACGCCGGG CCACGAGGAC TTCGTGCAGT
2051 GGGAGATGGA GGTGTGAAA CTGCCGCGC TCTCTCTCAA CGGGGTTCGA
2101 TTTAAGCGGA TATCGGGCAC CTCCATGGCC TTCAAAAACA TTGCCTCCAA
2151 AATAGCCAAC GAGCTGAAGC TTAA (SEQ ID NO:1)

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FIGURE 1A

FEATURES:

Start Codon: 1

Stop Codon: 2173

Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 18000005076710 /altid=gi 11067437 /def=ref NP_067731.1  ser...	1418	0.0
CRA 46000103792917 /altid=gi 15042611 /def=gb AAK82368.1 AF3876...	1384	0.0
CRA 117000066864950 /altid=gi 9845489 /def=ref NP_004945.2  ELK...	1379	0.0
CRA 18000005061736 /altid=gi 9845487 /def=ref NP_059672.1  ELKL...	1339	0.0
CRA 88000001156998 /altid=gi 7446398 /def=pir  G01025 serine/th...	1339	0.0
CRA 149000126080096 /altid=gi 14250622 /def=gb AAH08771.1 AAH08...	1332	0.0
CRA 18000004939026 /altid=gi 6679643 /def=ref NP_031954.1  ELKL...	1319	0.0
CRA 18000004906726 /altid=gi 346945 /def=pir  S31333 protein ki...	1248	0.0
CRA 32000237666055 /altid=gi 14764243 /def=ref XP_037764.1  ELK...	875	0.0
CRA 32000237666053 /altid=gi 14764237 /def=ref XP_037763.1  ELK...	875	0.0

Blast hits to dbEST:

CRA Number	gi Number	Score	Expect
CRA 56000140027815	gi 14649878	1604 bits (809)	0.0
CRA 113000033910976	gi 10216507	1463 bits (738)	0.0
CRA 160000136119317	gi 14173010	1417 bits (715)	0.0
CRA 113000033942433	gi 10219367	1417 bits (715)	0.0
CRA 107000020386558	gi 9343047	1255 bits (633)	0.0
CRA 158000041290072	gi 10994272	1223 bits (617)	0.0
CRA 11000545544945	gi 9155653	1187 bits (599)	0.0
CRA 225000001741704	gi 15755809	1158 bits (584)	0.0
CRA 160000136058139	gi 14169810	1152 bits (581)	0.0
CRA 1000491165793	gi 5452865	1130 bits (570)	0.0
CRA 11000545526171	gi 9153925	1059 bits (534)	0.0
CRA 78000106801247	gi 10390259	995 bits (502)	0.0
CRA 147000035349687	gi 12399257	979 bits (494)	0.0
CRA 112000056972111	gi 14374440	979 bits (494)	0.0
CRA 64000081152930	gi 15346261	948 bits (478)	0.0
CRA 11000545400890	gi 9142297	938 bits (473)	0.0
CRA 155000146359590	gi 13327757	922 bits (465)	0.0
CRA 11000545450274	gi 9146937	912 bits (460)	0.0
CRA 45000033524462	gi 8257100	910 bits (459)	0.0
CRA 47000019387182	gi 9775630	908 bits (458)	0.0
CRA 11000545400296	gi 9142242	890 bits (449)	0.0
CRA 118000028616173	gi 10901028	835 bits (421)	0.0
CRA 223000002472058	gi 15688546	690 bits (348)	0.0

FIGURE 1B

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

gi Number	Organ	Tissue Type
gi 14649878	brain	neuroblastoma
gi 10216507	lung	small cell carcinoma
gi 14173010	muscle	rhabdomyosarcoma
gi 10219367	lung	small cell carcinoma
gi 9343047	lymph	Burkitt lymphoma
gi 10994272	(none)	ovary, tumor tissue
gi 9155653	placenta	choriocarcinoma
gi 15755809	pooled colon/kidney/stomach	
gi 14169810	colon	adenocarcinoma cell line
gi 5452865	colon	colon tumor, RER+
gi 9153925	placenta	choriocarcinoma
gi 10390259	placenta	choriocarcinoma
gi 12399257	placenta_normal	
gi 14374440	colon	
gi 15346261	pooled pancreas/spleen	
gi 9142297	lymph	Burkitt lymphoma
gi 13327757	kidney	renal cell adenocarcinoma
gi 9146937	kidney	renal cell adenocarcinoma
gi 8257100	breast_normal	
gi 9775630	cervix	cervical carcinoma cell line
gi 9142242	lymph	Burkitt lymphoma
gi 10901028	uterus_tumor	
gi 15688546	Pancreas	Purified pancreatic islet

FIGURE 1C

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1  MSSARTPLPT  LNERDTEQPT  LGHLDSPKSS  KSNMIRGRNS  ATSADEQPHI
51 GNYRLLKTIG  KGNFAKVKLA  RHILTGKEVA  VKIIDKTQLN  SSSLQKLFRE
101 VRIMKVLNHP  NIVKLFEVIE  TEKTLYLVE  YASGGEVFDY  LVAHGRMKEK
151 EARAKFRQVV  SAVQYCHQKF  IVHRDLKAEN  LLLDADMNIK  IADFGFSNEF
201 TFGNKLDTEFC  GSPPYAAPEL  FQGKKYDGPE  VDWSLGVIL  YTLVSGSLPF
251 DGQNLKELRE  RVLRGKYRIP  FYMSTDCENL  LKKFLILNPS  KRGTLQIMK
301 DRWMNVGHED  DELKPYVEPL  PDYKDP RTE  LMVSMGYTRE  EIQDSLQVGR
351 YNEVMATYLL  LGYKSSELEG  DTITLKPRPS  ADLTNSSAPS  PSHKVQSVS
401 ANPKQRRFSD  QAGPAIPTSN  SYSKKTQSN  AENKRPEEDR  ESGRKASSTA
451 KVPASPLPGL  ERKKTTPPTS  TNSVLSTSTN  RSRNSPLLER  ASLGQASIQN
501 GKDSTAPQRV  PVASPSAHNI  SSSGGAPDRT  NFPRGVSSRS  TFHAGQLRQV
551 RDQQLPYGV  TPASPSGHSQ  GRRGASGSIF  SKFTSKFVRR  NLNEPESKDR
601 VETLRPHVVG  SGGNDKEKEE  FREAKPRSLR  FTWSMKTTSS  MEPNEMMREI
651 RKVLDANSCQ  SELHEKYMLL  CMHGTPGHED  FVQWEMEVCK  LPRLSLNGVR
701 FKRISGTSMA  FKNIASKIAN  ELKL  (SEQ ID NO:2)

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FEATURES:

Functional domains and key regions:

Prosite results:

PDOC00001 PS00001 ASN\_GLYCOSYLATION

N-glycosylation site

Number of matches: 4

1	90-93	NSSS
2	385-388	NSSA
3	480-483	NRSR
4	519-522	NISS

PDOC00004 PS00004 CAMP\_PHOSPHO\_SITE

cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 5

1	291-294	KRG
2	406-409	RRFS
3	444-447	RKAS
4	462-465	RKKT
5	702-705	KRIS

PDOC00005 PS00005 PKC\_PHOSPHO\_SITE

Protein kinase C phosphorylation site

Number of matches: 16

1	3-5	SAR
2	29-31	SSK
3	75-77	TGK
4	121-123	TEK
5	290-292	SKR
6	374-376	TLK
7	392-394	SHK

FIGURE 2A

8	423-425	SKK
9	442-444	SGR
10	449-451	TAK
11	479-481	TNR
12	537-539	SSR
13	584-586	TSK
14	603-605	TLR
15	628-630	SLR
16	634-636	SMK

PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site  
Number of matches: 8

1	10-13	TLNE
2	42-45	TSAD
3	75-78	TGKE
4	133-136	SGGE
5	275-278	TDCE
6	338-341	TREE
7	366-369	SELE
8	639-642	SSME

PDOC00008 PS00008 MYRISTYL  
N-myristoylation site  
Number of matches: 5

1	348-353	GQRYNE
2	559-564	GVTPAS
3	574-579	GASGSI
4	610-615	GSGGND
5	706-711	GTSMAF

PDOC00009 PS00009 AMIDATION  
Amidation site  
Number of matches: 3

1	222-225	QGKK
2	442-445	SGRK
3	570-573	QGRR

PDOC00100 PS00107 PROTEIN\_KINASE\_ATP  
Protein kinases ATP-binding region signature  
59-82 IGKGNFAKVKLARHILTGKEVAVK

PDOC00100 PS00108 PROTEIN\_KINASE\_ST  
Serine/Threonine protein kinases active-site signature  
171-183 IVHRDLKAENLLL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	231	251	1.431	Certain

BLAST Alignment to Top Hit:

>CRA|18000005076710 /altid=gil11067437 /def=ref|NP\_067731.1|  
serine/threonine kinase [Rattus norvegicus] /org=Rattus  
norvegicus /taxon=10116 /dataset=nraa /length=722  
Length = 722

Score = 1418 bits (3629), Expect = 0.0

Identities = 706/724 (97%), Positives = 715/724 (98%), Gaps = 2/724 (0%)

Frame = +3

Query: 396	MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNMIRGRNSATSAD	EQPHIGNYRL	LKTIG	575
	MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNM+RGRNSATSAD	EQPHIGNYRL	LKTIG	
Sbjct: 1	MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNMLRGRNSATSAD	EQPHIGNYRL	LKTIG	60
Query: 576	KGNTAKVKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIVKLF	EVIE	749	
	KGNTAKVKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIVKLF	EVIE		
Sbjct: 61	KGNTAKVKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIVKLF	EVIE	120	
Query: 750	TEKTLYLMEYASGGGEVFDYLVAGHGMKEKEARAKFRQVSAVQYCHQKFIVHRDLKAEN	929		
	TEKTLYLMEYASGGGEVFDYLVAGHGMKEKEARAKFRQ+VSAVQYCHQKFIVHRDLKAEN			
Sbjct: 121	TEKTLYLMEYASGGGEVFDYLVAGHGMKEKEARAKFRQIVSAVQYCHQKFIVHRDLKAEN	180		
Query: 930	LLLDADMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPELFQGKKYDGP	VDW	SLGVIL	1109
	LLLDADMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPELFQGKKYDGP	VDW	SLGVIL	
Sbjct: 181	LLLDADMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPELFQGKKYDGP	VDW	SLGVIL	240
Query: 1110	YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSKRG	TLEQIMK	1289	
	YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSKRG	TLEQIMK		
Sbjct: 241	YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSKRG	TLEQIMK	300	
Query: 1290	DRWMNVGHEDDELKPYVEPLPDYKDPRRTELMVSMGYTREEIQDSL	VGQRYNEVMATYLL	1469	
	DRWMNVGHEDDELKPYVEPLPDYKDPRRTELMVSMGYTREEIQDSL	VGQRYNEVMATYLL		
Sbjct: 301	DRWMNVGHEDDELKPYVEPLPDYKDPRRTELMVSMGYTREEIQDSL	VGQRYNEVMATYLL	360	

FIGURE 2C

Query: 1470 LGYKSSELEGGDTITLKPRPSADLTNSSAPSPSHKVQRSVSANPKQRRFSDQAGPAIPTSN 1649  
LGYKSSELEGGDTITLKPRPSADLTNSSAPSPSHKVQRSVSANPKQRR SDQA PAIPTSN  
Sbjct: 361 LGYKSSELEGGDTITLKPRPSADLTNSSAPSPSHKVQRSVSANPKQRRSSDQAVPAIPTSN 420

Query: 1650 SYSKKTQSNNAENKRPEEDRESGRKASSTAKVPASPLPGLERKKTTPSTNSVLSTSTN 1829  
SYSKKTQSNNAENKRPEE E+GRKASSTAKVPASPLPGL+RKKTTPSTNSVLSTSTN  
Sbjct: 421 SYSKKTQSNNAENKRPEE--ETGRKASSTAKVPASPLPGLDRKKTTPSTNSVLSTSTN 478

Query: 1830 RSRNSPLLERASLGQASIQNGKDSTAPQRPVASPSAHNISSSGGAPDRTNFPRGVSSRS 2009  
RSRNSPLL+RASLGQASIQNGKDSTAPQRPVASPSAHNISSS GAPDRTNFPRGVSSRS  
Sbjct: 479 RSRNSPLLDRASLGQASIQNGKDSTAPQRPVASPSAHNISSSGAPDRTNFPRGVSSRS 538

Query: 2010 TFHAGQLRQVRDQQNLPGVTPASPSGHSQGRRGASGSIFSFKFTSKFVRRNLNEPESKDR 2189  
TFHAGQLRQVRDQQNLP+GVTPASPSGHSQGRRGASGSIFSFKFTSKFVRRNLNEPESKDR  
Sbjct: 539 TFHAGQLRQVRDQQNLPGVTPASPSGHSQGRRGASGSIFSFKFTSKFVRRNLNEPESKDR 598

Query: 2190 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSSMEPNEMMREIRKVLDANSCQ 2369  
VETLRPHVVG GG DKEKEEFREAKPRSLRFTWSMKTTSSMEPNEMMREIRKVLDANSCQ  
Sbjct: 599 VETLRPHVVGSGGTDKEKEEFREAKPRSLRFTWSMKTTSSMEPNEMMREIRKVLDANSCQ 658

Query: 2370 SELHEKYMLLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRISGTSMFAKNIASKIAN 2549  
SELHE+YMLLC+HGTPGHE+FVQWEMEVCKLPRLSLNGVRFKRISGTSMFAKNIASKIAN  
Sbjct: 659 SELHERYMLLCVHGTPGHENFVQWEMEVCKLPRLSLNGVRFKRISGTSMFAKNIASKIAN 718

Query: 2550 ELKL 2561  
ELKL  
Sbjct: 719 ELKL 722 (SEQ ID NO:4)

#### Hmmer search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	346.8	2.3e-100	1
CE00022	CE00022 MAGUK_subfamily_d	59.5	1.8e-17	3
CE00359	E00359 bone_morphogenetic_protein_receptor	19.6	7.5e-05	2
CE00334	E00334 urotrophin_receptor	12.7	0.00057	2
PF00627	UBA domain	12.5	0.096	1
CE00031	CE00031 VEGFR	4.0	0.25	1
CE00203	CE00203 ERBB_RECEPTOR	3.0	1.7	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-16.2	3.4e-07	1
CE00292	CE00292 PTK_membrane_span	-21.5	6.9e-08	1
CE00291	CE00291 PTK_fgf_receptor	-35.7	1.2e-06	1
CE00290	CE00290 PTK_Trk_family	-65.9	5.2e-11	1
CE00289	CE00289 PTK_PDGF_receptor	-68.0	0.4	1
CE00286	E00286 PTK_EGF_receptor	-75.9	1.8e-06	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-179.5	1e-06	1

FIGURE 2D

CE00288 CE00288 PTK\_Insulin\_receptor -208.8 0.01 1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00022	1/3	59	131 ..	23	98 ..	10.3	0.0061
CE00359	1/2	54	141 ..	142	233 ..	5.7	0.64
CE00289	1/1	52	155 ..	1	109 []	-68.0	0.4
CE00022	2/3	157	183 ..	128	154 ..	14.5	0.00034
CE00031	1/1	172	195 ..	1068	1091 ..	4.0	0.25
CE00203	1/1	171	195 ..	861	885 ..	3.0	1.7
CE00334	1/2	172	197 ..	678	703 ..	11.1	0.0018
CE00359	2/2	171	201 ..	272	302 ..	14.5	0.002
CE00334	2/2	230	240 ..	738	748 ..	-0.3	7
CE00288	1/1	55	281 ..	1	269 []	-208.8	0.01
CE00022	3/3	211	292 ..	188	271 ..	34.3	4.9e-10
CE00290	1/1	54	302 ..	1	282 []	-65.9	5.2e-11
CE00291	1/1	53	302 ..	1	285 []	-35.7	1.2e-06
CE00286	1/1	53	302 ..	1	263 []	-75.9	1.8e-06
CE00292	1/1	53	302 ..	1	288 []	-21.5	6.9e-08
CE00287	1/1	53	302 ..	1	260 []	-16.2	3.4e-07
PF00069	1/1	53	304 ..	1	278 []	346.8	2.3e-100
PF00627	1/1	332	362 ..	9	41 .]	12.5	0.096
CE00016	1/1	2	412 ..	1	433 []	-179.5	1e-06

FIGURE 2E



1 TCTAGGCGGG GAGACAAGCT CAGCAGCCTT GTGCAAAGCT AGCAAGGAAG  
51 AGAAAGGATA GGTAGGGTAG GGGTTGGGGA TGAAGGTCAA AGGGCAGGGG  
101 TGAGGCAGGG GTTAGAGCTA GAGTGAGAAG CTTGGAGAAG ATGGAGTCTA  
151 TTTAGACGAG AGTGTGGACC AGGGAGAGAC TGCTGGAACA CCAACCACCA  
201 ACTGCTTCCT CTCTCTTTTC CCTGCTTTCC AGACCCTGGC ATTAGAGGTG  
251 ATACCAGGCA CAGGAATCAG CAACGTGTCT CCCTTTGGCC ACCAGAGGGC  
301 AGATGATTCT CAAGGATCGA ATTTGGGTTG GGGAGTGAGG TGTTCTCTGT  
351 CCTCCTCTTC TCTCTTTCCC TCACCTTCAT GGGTGTGCCT TCACCTTCTT  
401 CCTCAACGGT TGGGTGCCTG AATAGAGCTG GTATGGGGCA TGGGGAGCAG  
451 TGCTGAAGTC CCAGGATTTA CTAAGAGTGT AGTGATACCT GTTGCCTTAG  
501 GAAGTACTTT CATAACCTGG TAATTACATC TGCTCAGATG CCTATTTCTC  
551 TGATTGATGG GATGAAGGCT GGCTCAAGAT GCTGTAGCTG GGAGTTGGAG  
601 GTCAAGTAGC AGGGGTCCAA TCAGCAGTTT TCCCAATAAC TCCTGGAGCC  
651 TCTCTGCTCC TGTACCTTTG GGAACCTGTT GCCTGAGTCT GGTTTCTGAC  
701 TCCTGCGGGG CCTCTGCCTC CTGCCACCT TAAGCCACTG ATGGGAGGGT  
751 GTGGTTCCAA CGTGTTCCAG GTACTATGGG TGAGGACAGC TTGGCGCTGG  
801 GGAAATCAGC CCAGGATACT CCCTGTCCTT GGTAACGCAG TGTAAGGGGA  
851 AGTGAGGAAT GGACTGCACT TGCCATACAG ACTTCCTGTT AGTCAAGGGC  
901 TCTCCAAAGC TGAGAAGGAC CTCCGAGTTC ATGAATCCAA TGGCTTCACT  
951 TTA CTGATGG GGA AATGAG GCCCAGAGGA GGAAAGAAAA GAAACTTTAA  
1001 ATGCCTTATC TTGCAGAGGC ATTTTAAAAG GTA ACTGGAA TTCAGAAATG  
1051 TCATTTTGAA TGTCAACGCA GGAGCAAAGG CAAAGGAAAG AGGAGCCTAA  
1101 ACTCAGTGAT GTTATGTGAT TTTTCCAAGA TCACGCAGCA TTGGCACTTG  
1151 GCAGAGCTGG GGCTGAAATG CAGGGCCCTG GACGCTCCCG CATCCGGTGC  
1201 AGAGGACGCT GCCCTGGGCC TGCCTGGGGC CTTGCCGAGC CCTGCGGACT  
1251 AGATGCGGGA ATGCACGGAT GAATCCACAG AAGCCAAGAT AGACGGTGGC  
1301 AGACAGGCAA TAGACTGATG CTGCATTGA CAGGTATATT GATAGGCTAG  
1351 ATGATAAAAA GAAGATGAAT TTTATGAGCT GACCGACAGA TGGACAGAAA  
1401 TGCAGACAGG AAGCTGCTAT AGAACCAGAG GATGCCAATC ACAGGGACGG  
1451 CTAACAATCT TGT TTTGTAT TTAGTCAAAT CACAAGCACA GACAGGTGAC  
1501 CCACGCTTCC TGT TCAAGT TGA AATGC CCGAAA ACTG ACGGAAAGAC  
1551 ACGAAGCGAA TCAGACTCCG AGAGCCACCC GGGGAAACGA CCGGGTGCTC  
1601 GGAGGGCCTC GGGTGTGTC GGA AATGGC GACGACCGCC CTCGGCAGGG  
1651 CTGTGGGAGG GGGCGTGGCC GGCTCAGCAC GCGGAGCAGC TTCGGGTATT  
1701 TCCGGAAACT GCCGAAAGCC CCCTTGAAGT GGGCGGGGAA AGGCCGGTGG  
1751 GCGTGGCTGG ATGGCCGTGG ACGGGGGCGG GGGGTAGGCA CCCGGGGTCG  
1801 CTTCTGGAT TTCCGTAAAC AGAGCCGAAG CTTCTGCTTC GGAATCGAGG  
1851 AGGAGAGCGC GTCCCCGGGG TTTACCTTCT TCGGCTGTTT CCGGAATTCA  
1901 CCCGTAGTCT GTGGCCGGGA GGAGAAGGCG CGCCCCACCT CCCGTTTCTA  
1951 GCCGCTTCGG ATGTTTCCGG CTGCTGCCGG CGAAAAGAGC CGAGGGCCGG  
2001 CGGTGGTGGC GGCCATGTTG GGAGCAGCAG GTCCGGCGGC GGCTGCCTGT  
2051 GTGCCGGGCG CGGAGCAGTG CCGCTGAGGG CAGGGGAGGA GCGAGGCAGG  
2101 CGGCCGGCTG CGGCGGCAGA GAGTAGGCGG AGCGGCGCGG CCCGGCCGAA  
2151 AGGCGGCACA GCCCAGCCGG GGGTCGGGGG GGTGCGGTCC GGAGCCGCTC  
2201 GGAGCCGGCG CGGCCTAGCC CGAGCGGCGC ATCCCCGGGC TGGCGTGAGC  
2251 GGCTGCCCGG CCTCCCCGCA CCCCCGGCCG GGGCCCATGC GGCGGGTGCT

FIGURE 3A-1

2301 CCTGCTGTGA GAAGCCCCGC CCGGCCGGGC TCCGCGCCTT CCCTTCCCTC  
2351 CCTTCCTCCA AGCTTCTCGG TTCCCTCCCC CGAGATACCG GCGCCATGTC  
2401 CAGCGCTCGG ACCCCCCTAC CCACGCTGAA CGAGAGGGAC ACGGAGCAGG  
2451 TAAGGAGCCC CGAGGGCTCC CCGAATTCTC TGGCTGGGCC CTTTGCACCT  
2501 TGCGGAGCCT CCTCCCTCTT CTGCTCTCCT CGTGCCCCCTG CTGCCATCCT  
2551 GCAAGCCTCG GCTGCCCTGT CATCCGGCTC CTGGCTCCGG CTCCGCACAT  
2601 CCCGCTTCCG AGTCCTGACC TGGGACCCAC CTCGTCCTGA CTCCAAGCTG  
2651 CACACTTGTC TTTCTGCCAA CCCCCGTCTC CCCTCACCGC CCTCCTGCGC  
2701 TCTTCCGTGT CACCTCCCCA GCTTCCCTTT CTCTTCCCTT TTTCTCTCAG  
2751 GGGCCTTTCT GGTCTTCTCT CACCCACGCT TAAAGCAGCC ACCCTCCCGC  
2801 TCCTCGAATA GCAGCACCCC GCGATTTGCC ACAGATCGTT GTCCACCTCT  
2851 CCCTTCGTCT CTCCTGCCTC GCTTCCCCTC CGCCCGCACC GGTTCGCA  
2901 GTCTCTGGGT TATCACCTC AGGGTCCTTG CCCTGGACTG CGCTCTCGAT  
2951 CCCTGGCCCC TTGCAGTTCC CCCAGCTTTT TCTACCCTGC TTCTTCGTTT  
3001 TCCAAATTGT GCTCTCCCTC TTGCTTGCAA CCCACCAGCT CCACCCTCAT  
3051 CACCTTTCCA AATCCTTCGC CTACTCTTTG CTCATCACTT TCCCTTCTTT  
3101 GCTCCAGGAG CTCCCTGGAT CCTGGCGCTG GCATTTGTCTG CTTCCGTGTT  
3151 TCCCCACAGC TGTATGCGC ATAGTTTTCC CACAGGTTGC GTTTGGGGTT  
3201 CCAATCATCA CTCCCTTCAG AGTCTTTGGA TCCCTCTTGT TCTCTTCCCC  
3251 TCGGGTTTGG CTTTTAGGTC CCTGGGCCCTC TTGTTTCTCT CTGTGAGTGT  
3301 TCTACCAGCC TTCTACTGGG CTCTTTCTCC CAACCCAAAG ACACTTGGCC  
3351 CCACCGTATT AACACAACCT GTTGCTCAGT CCTTTCCAG ACCTCGCTGC  
3401 ATCACAGTTT TTGCCTTTCT GTCTTCGTAC GCTGGAACAC AAACCATGAT  
3451 GACTTTCTGT GTCTTCACTC CCGTGCCTGG CACTTAGAGT ATTTTCTTTC  
3501 TTGCTTGTG CTTTCTGTG TCTCCACCCT CACCCCATCT TCCTTACTGT  
3551 GCCTTTTAAT CAGCGTTGCC TTTTCTCTCC GCATTAGTCT CCTGCCTTCT  
3601 TCATGTCCTG TGTATCCCCA CACCGTGCTT GGATCCATTC TGTTCTTATT  
3651 GGCTAAGTCT CTGTAATGCC CAGGAAGTCC AGGTGTTTTG CATGCTAGTT  
3701 TCTTGAGCTA CACCTCAGCC TCACGACTCT ACACGGTCCC CCTCATCCTG  
3751 GCAGTCACTG CTATGTTTTT CACCCAAGTC TTAGCCTTTC TGTGTCATCT  
3801 CACTTTTGAT CCCAGAGACG TCCACTTTCC ACACCTCCCC TTTATTTTAC  
3851 CATCTCTAGC GTCCTTTGCT GACTGCTCTG TGCAGAGTCC CCTGCCTGTC  
3901 ATACCTTTCT TGGTGGAGAA CTTTACTAGG CCAAAAAAAC TTGACTTGAA  
3951 AAAGAAGTGC TTCTGCCCCG GGGCTGCTGT GCTTTTGGCC TTCTTTCCCC  
4001 TCCTTCCATC CTTTATGTTT CCCTCTTACT CCCTTCTTTC TTTGTAGCCC  
4051 GGTAGAGCAG TTGTTGTATT CTCTTGCATG TGAACATTCT TCTTTGAAAA  
4101 ATCTTACCTC CTTTCTTTTA CTGTGTTTTT CTATTTTGTG ACCCCCTGGC  
4151 CCTCTGTCAC CTGGGCAGTT AGGAACTAAA GAGAAGTTCT AGGCAGAGTT  
4201 TTTCTCTGCA GGGTTGACCC TTTTATTACT TGTGGATTAT TTGCTTCTGG  
4251 GGGTGAAATA GGGGTTGAGA GGGAGGGATG GTTGATTTC ATTTTCATCAC  
4301 TGGGTTTGGC AGCTGGTTCT GCATGGGACA GGGGTCCTTG GAGACAGAGG  
4351 AGCATGTTCT GTGTCTCGCA GTCTTCTCT CCCTTGCCTA CCGGCTGTTT  
4401 CTCTCTCCTT ACTGGGAATT GCTTCTCTG GGCCCTCTG AGGTTGCTTA  
4451 TTCCACCCAT TTTCTCTCA CAACCTTTGT TTAGCAGGT AAACCCTGCT  
4501 TAACCAGAGA ACTTTCCAG ACTGTTGATC GTGAGCTGGT AGGAGGAGGC  
4551 CAAGTGACTG ACTGGCACCC TCAGGCATTT GGGGAGTGCC GATGGAGTGC

FIGURE 3A-2

4601 CTA CTCTCAG TGAGGCTGGT GGGGGGCATT GTGTTCAGCA GAGCAGAGTA  
4651 ACAGACTGCC TCAGTGTGGT TTCTTTGTGC TGCTTACTAC ATGTAAATGT  
4701 ATTATTGCCA TGGTATTTTT CCTGTGATGT GTGTGTTGAT TTCCTTTCTT  
4751 CCTTACATGC CTAGCATACT GCTGAGCATA TAGTAGGAAT TCCACCGTAG  
4801 TGTGCATCCA CTGATTCCAT GATAGCAGCA ATCAGTGACC ATTTGGGAAT  
4851 GTAAGTAAGC TCTTTGCTCT TTGATAACTT TGCCCAGAGC AGTAGCTGCA  
4901 TACATTGTCA TCCTGTTAGG ATTATTAATT ACCCATCCTA TTTCTACTCT  
4951 TTATGGACTT AGATTCTCCT TAGCCCCTTC ATACCTTCTA CTGTTGTTCT  
5001 CAGGGTAGCC AGTCACTGTA TCGATTTAAT ATTAAGTCTC ATTCCAGTAA  
5051 AAGCAGGGAC TTTGGA AAAAC CTTGGATGCA CCTATTCCAG ACAGATTCTT  
5101 GTATTCTTTT TTTTTTTTTT TTTTGAGATA GAGTCTCGTT CTGTCGCCAG  
5151 GCTGGAGTGC AGTGGCACAA TCTTGGCTCA CTGCAATCTC CGCCTCCTGG  
5201 GTTCAAGCGA TTCCCTGCC TCAGCCTCCT GAGTAGCTGG GACTACAGGC  
5251 ACACACCGCC ACGCCCGGCT AATTTTTTGG ATTTTAGTAG AGACAGCGTT  
5301 TCACCATGTT GTCCAGGATG GTCTCAGTCT CCTGTCTCG TGATCCGGCC  
5351 TCCCAAAGTG CTGGGATTAC AGGTGTGAGC CACTGCGCCG GGCCTGATTC  
5401 CTGTATTCTT TAAAACGGGA AAAAAGACAA GCAGCAGCTC CTCAGGTCAC  
5451 AAGGCCAGGT ATATCAACA CTGGCCTCCG AGAATAGATC ATGCCACCAA  
5501 GTGAAAGAAA CCTCTTCTTG GTCCTGTTGT GATTTTAGAT AAAGTAGTCA  
5551 TGGAAGCTTG GTCATTACTA TAGTCTTAAT GTTATTTTTT TAAAAAGGG  
5601 GATTTAGTTG GGCTGATTTC CTCCCCTAAA GGTCTCTGT CACCTTATTT  
5651 AAATTTAAAA CTGGTTTTAC CAGAAAATAG GTAAACAAAC ACCACTGGTT  
5701 GTCTCCAGTC TCTTTTCTTG CTCTTCCTCT CCCTCTTCTT TAAAAATGTG  
5751 GCTGATGAGA ACCTGTTTCC AGGAGCCCTT TAATCACTCT GAAACACACA  
5801 GACACTGAAA ATGTTGAAGC ATAAAAATAA ACCTTGCGTT ACAGGGAGAT  
5851 TGCCTGTGTG CTGTCCACTT CGCTTATAAC AGTGAAAGTA GGAGATTAAA  
5901 AAAAAAAAAA AGTTAAGCCC TGTCTTTAAG ATGGTTTTTG TGACACCTGA  
5951 TTCCAGATGT GCTTTTTTAC AGCCATAGAC TTCCTGCTTT TGCAGAAGGA  
6001 GGGTTCTAAT CTGGGGCTCG TAGCTTGGGG GATTCTTAGT TTGTGAGCTG  
6051 AGCTTTTTGT TCACTTCTTT TCCAAATGAC TCTGCTGGCC TGAAGCTTGG  
6101 CAGTTGTGAA AGCAATCAGC AAGATGACTG TTTGTCTTCC AGCCAGCAGC  
6151 AGCAGTCACA GGCAAGCCTG GAGAAAGGTC CAGCTTCCAG AGTTCACCTG  
6201 CTAGAGTTTT CCATAACACC TGGGGGAGAG GCTACTCCAT CTGGGACCTG  
6251 CCCCACCTCT GGGCCTCAGA AACTATGAGA GAGGGATTGA GAGAAAACCT  
6301 GCCCCACTTC TGCTGCAGTG GGAAGGGAGG GGGCTGCTGT CAGGCTTCTA  
6351 GGCAGTGAGC GGCATTGTTT ATTCTCTCAG TTCTAGGAAG GGGAGTTTAG  
6401 AAGTACTGGT GAAGAAAACA AAGTTACAAG ATCCTATAAG GAACAGCTGA  
6451 ACTACTCCAA ACACTCTCAC TGGACCCCA TTGTTGATTG TGGATAAAAA  
6501 TATATATATA TATAAACTC TTTTTTTTTT TGACACAGAG TCTTGCTCTG  
6551 TCGCCAGGC TGGAGTGTAG CGATGCGATC TCGGCTCACT GCAACCTCCG  
6601 CCTCCCGGGT CAAGCGATTG TCCTGCCTCA GCCTCCTGGG AGTAGCTGGG  
6651 ACTACAGGCG CCCACCACCA TGCTGGCTAA TTTTGTATT TTTAGTAGAG  
6701 ACGGGGTTTT GCCATATTGG CCAAGCTGGT CTCGATCTCC TGACCTCAGG  
6751 TGATCTGCTG GATAAATATT TTTTTTTTGC TTTTGGTGTA ACTTAGGTAG  
6801 ATTGATCGG CTAGCTAGCA TCTCAGTCCA CACTCTGAGC TGTGCAGCAG  
6851 TGTGCCCTGG TGCTAATTCT CACTCTGTCC TTTGATTCTG GCCAGGGGGT

FIGURE 3A-3

6901 CCTTGGTGGT GCTGCCTTCT GGTGAGGAAT GTGGGTGAAT GTCAGACCAA  
6951 ATAGTGTAC TTTGGGCTTG GCCCTAGAGA TCAGGAAGGA AGTGTGTGTA  
7001 GAGCAAGGGC TTTGGGAGTC CTTGGAGTTC GTAACCTTTG AATCTGAAAA  
7051 GAACTGTAC CTAGTAAATT AGAATAATTT CTCTCTGGTC AGGCACCATG  
7101 GCTCATGCCT GTAGTCCTAG CACTTTGGGA AGCCAAGGCA GGAGGATTGC  
7151 TTGAGGCCAG GAGTTCAAGA CCAGCCTGAT CAATAAAGTG AGACTCCATC  
7201 TCTACAAAAA AATTTTTTTA AATTTAGCTG GGCATGGTGG CACATGCCTG  
7251 TGGTTGCAGC TACACAGAAG GCTGAGGCAG GAGGATGGCT TGAGCTGGGG  
7301 AGGTCGAGAC TGCATTGAGC TGTGTTTGTG CCACTGCACT TCAGCCTGGG  
7351 TGACAGAGCA AGACACTATC TCAGAAAAAA AAAATTACTT TTCTCCAATT  
7401 TATGGACTTC GGAAAGTAGC TAAACAGATG GATATAAGAC AGTTGTTGAA  
7451 ACTCGGCCTG CTGCAGATTA AAATAAAGTT TGCACAAGGA TAACTTAATC  
7501 TTTGAGACCA ACCAAAGTTT GGGCTGGAGA TTTTCTCAG CATAAATGTC  
7551 CTAAGCAGAG TTGGTGCCTA TGAGGTAGGA AAAGATTGAG ACTTTGCTTG  
7601 CCTAAGAGGT TTGCAGGGT CGAGCTTTTG GGAGTCAGAA CTTCTCAGAC  
7651 TAGATTGTTT CCCCTTTGGA CAGAACAACC CAATTCTCAG TGGGCATTTG  
7701 ATCAGGACTA ACCCAGGCCT TCATGAACTC TTTCCCATG AGCACTTAGC  
7751 CACCTGGCTG GCATTTCTCT TCTCCAGGA GCTTCCATGA GGTTCCTACT  
7801 TATGTATTAT GTCGACTTGA ATGAATATTT TATGTCTAGA GTGCAGCCAA  
7851 GCCTCAGACT TTGTGGCCCA TTATCGACAA ATGGGGTAGG GGGTGGGCGC  
7901 CACCTTTGGC CCCGTGATAG CTTCTCTGCT AAATGGACTC CCCCAGCAG  
7951 CACTTTGAAG CCCATTAATG GATTGGAATG AAGTAACCTC AGCAGATGGA  
8001 AAGGGTGAGG AGGGTGGTCA TCTTCCTTCC CTGAGACTGC CTGATGAGGC  
8051 TTTCTACAG TAACCAGGAC AAGCCCCTAT TCCCTCTGCT TGGTTAAGCT  
8101 GTGGACTGGA GCTACTAGGC CTCTGCTTTG AGAGGAAGTA TAGAAAGGAT  
8151 TTGATTCTCT TTTAGCCATG GTGGGGCCGC CAGTTTCCCC ACTTTCCCAT  
8201 CAAAGCAAAA ATTGAGAAGG ATGTGGAAAG GGTGGGTGGA GTTTAAAGCT  
8251 GGCCCTTCCT CCTTCAGTGG AAGTTCAGCA AAATGACAAA CCAGATAGGT  
8301 GGCTAAATTT CTTCTCTTG ATGGGAGATT CCAGTATTTG TACGTTTTGT  
8351 GCTTGTAGCT TGGATTCTCC AGGCCTCCTC CCAGCTTTCA TCAAACATGA  
8401 GTGAGTCACT GAAGTGTGT CTATGCATTT TCTCCCTTCT GTCTCTGCAA  
8451 AGGGAAGAGT AAGCCTTTAC AAACCTGTGG GGGAGGAAGT CACCCTCTTC  
8501 CCACTGCTGG AGAGCCAGGC TATCCCCAGG TTAACCCTGA AAGTGCTAAC  
8551 TCCTGAGCAG AATGTTACTG CCACCCGCCC CTTTCTTTT TGTATAGGC  
8601 CATTGAAGGT CATTGCTCGT CTTTTTTTTT GAGACAGTCT TGCTCTGGTC  
8651 ACCCAGGCTG GAGTGCAGTG GCAGGATCTC AGCTCACTGC AACCTCCACC  
8701 TACTGGGTTC AAGCGATTCT CATGCCTCAG TCTTCCAAAT AACCAGGATT  
8751 ACAGGTGCGC ACCTCCATGC CTGGCCACTT TTTGTATTTT TAGTAGAGAT  
8801 AGGGTTTCAC CATGTTGGCC AGGCTGGTCT TGAACCTCTG GACTCAAGTG  
8851 ATCCGCCTGC CGTGGCCTCT CAAAGTACTG GGATTACAGG AGTGAGCCAC  
8901 CGCGCCCGGC ATCATTGCTT ATCTTTTAGA CTGAGATAGT ACAGCTGATT  
8951 CTAACAGCA CCCAGAGAGA ATCTGGCCTC TTGATTTCCT GTTGTTCTC  
9001 AGAGGAGGAG GCATCCAGT TCCTCCTCTT GCCCTCTAGA CATCTCCTCC  
9051 TCTGATAAGT ATAAATAGGC TAGATCCCTT TATCTTCATA TCTGTTTTTG  
9101 TCTGGAATGT TTCAAGTTTC TCAAGCTAGG TGTGGTGGCT CATATCTGTA  
9151 ATCCCAGCAC TTCGGGAGGC CACGGCAGGA GGATCACTTG AGCCAGGAG

FIGURE 3A-4

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9201 TTCAAGACCA GCCTGAGCAA CATAGTGAGA CCTCATTTCT ACAAAAAAAAA
9251 AATTTTTTTTT TTGAGACAGT CTTGCTCTGG TCACCCAGGC TGGAGTGCAG
9301 TGGCAGGATC TCAGCTCACT GCAACCTCCA CTTACTGGGT TCAAGCGATT
9351 CTCATGCCTC AGTCTCCCAA ATAGCTGAGA TTACAGGTGT ACGCCACTAT
9401 GCCTGGCTAA TTTTGTATT TTTAGTAGAG ATGGGGTTTC ACCATGTTGG
9451 TCAGGCTGGC CTTGAACTCA TGACCTCGTG ATCTGCCTCA GCCTCCCAAA
9501 GTGCTAGGAT TATAGGCATG AGTCACCCCG CCTGGCCAAA AAAAATTTTTT
9551 TTTTTTTTTT TGAGACGTTG TCTTGCCCTG TCGCCAGGC TGGAGTGCAG
9601 TGGCACGATC TCGGCTCACT GCAAGGTCCG CCTCCCGGAT TCACGCCATT
9651 CTCCTGCCTC AGCCTCCCGA GTAGCTGGGA CTACAGGTGC CCGCCACCAC
9701 ACCCGGCTAA TTTTTTGTG TTTTCAGTAG AGACGGGGTT TCACCTTGTT
9751 AGCCAGGATG GTCTCGATCT TCTGACCTCG TGATCCACCC ACCTCGGCCT
9801 CCCAAAGTGC TGGGATTACA GCGGGGAGCC ACCGCGCCCA GCCCAAAAAA
9851 ATTTTTAAAA AGTTACCTGG GTGTGGTAGC ACATGCGTGT ATCCCACCTA
9901 CTCAGAAGGC TGAGATGTGA GGATCACTTG AGCCTGGGAA GTTGAAGGCTG
9951 CAGTGAGCTG TGATCATGCC ACTGCATTCC AGCCTGGGCA ACAGAGTGAG
10001 ACCCATCTC AAGATAAATA AGGTTTGTCA GTCCCTGTGG TGGTCTTTTC
10051 CGCAGATGTC TGTCTTTGGG TTGGCACTTA TTCCCTCTA CTTCAGTTA
10101 TTCCTTACAT TTCTCATTAG AAAATGGCAA AAAGGGCAAA AGTAAATTCA
10151 TTTCTTTTTT ACACCAAATC ATTAATTTTA GGCTTATAAA ACTAAATGAA
10201 CAGAAGATTT GGTAGGAGAG GAGGGGAGAT GGACACTGAT ACTGGTGGCT
10251 AGGTGATCCT GAGGGACAAC TGGTGCCTGG CAGAAAGAGA GGAGGGCTGT
10301 GTTCAGTGAC TGGCTCCCAG CCACCTTTTT GGCCTTTTTC TTTTAAACAT
10351 GAGGAAGGCG GAGCAGACCA GGGGCTTCTC TGTAGAACCA GTCAAGCTGG
10401 TTTTGGGCAG CCTTGGCCTA TTTCTTTGTG TGCTCTTTGG GAAGTTGGCA
10451 ATACAAAGGT CTGCCTCCTT TGGGGCTGTG TTCGTTGAGG CGAAAGTTTG
10501 GAAGACAACCT ATCTGTCAAC AACCCCTTTC TCCCAAAACA CTGAATGGGT
10551 CTCTGAGCTG GTCCTTCACT CCAGGGAGGA GGCTTTCTCT CCACCCTATG
10601 CTGAACCTGA AGGCAGCTTT GCTTTATACA CTTTCACTG AAAGCTCTAA
10651 GACATTAACCT CTTTTTTTGG ACTCCCTTCC CAATTCACAA CTTGGTGAAA
10701 GACCCTCAGC CTAGCCAGGA GGAAGGGACT GGGTCTGCCT TTGGCTCCTC
10751 ATTTATGGGT CTGGGAGGGG ATCAGGACTC CTTACTGCTA TGATCTGGCT
10801 GCTAAATTCA GTGACATCCC AGGCCTTTTT TCGTCCACGC AATGGGACTG
10851 TCTGTCCAGG CCTGCTGGGA AAGAAAAGAG AGAAAAAATA GTTTTTGCTC
10901 TTTGGCAGCT TACAGGGACT TCAGCCATAG GAAACAACCT GTAGGAAAGG
10951 TGGGAGCTTC CGGTCACCAT GTGTGCTGAC ACTTCTGCA ATAGCACTAG
11001 GGAGTCTTTC TCAGGGAGCA AGGCCAGCCA GGTAGGATTA TTTCCAGTC
11051 TCCCAGCTAA GCAGGAAATG CCAAATATG AACGTTTAGT AATTAGTGAG
11101 TGTAACCTACC TGCTGACAGA GCTCCAGCCT AGACCTTGTC CTTGGGGGCT
11151 GGTTGCCCCT GTTGATACTA CAGTGAGCTA CTCATTGCTT CTGATTACCA
11201 TTTCAGTATG AGTTTTGCTT TGGTTTCTGA TATCCCATGT GCGGCTGCCT
11251 TTTTCTCCA CTTCTTTTTT GTTGTGCTT TTTGTTTTTT TGAGACGGAG
11301 TCTTGCTCTG TTGCCAGGC TGGAGTACAG TGGCACAATC TCAGCTCACT
11351 GCAACCTCCG CTTCCAGGT TCAAGCAATT CTGCCTTAGC CTCCAAGTA
11401 GCTGGTACTA CAGGCATGTG CCAGCACACC CGGCTAATTT TTTTTTTTTT
11451 TTTTTTGAGA CAGGGTCTCG CTCTGTCGCC CAGGCTGGAG TGCAGTGGCG

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FIGURE 3A-5

11501 CGATCTCAGC TCACTGCAAG CTCTGCCTCC CGGGTTCACA CCATTCTCCT  
11551 GCCTCAGCCT CCCGAGTAGC TGGGACTTCA GGCGCCCACC ACCATGCCCCA  
11601 GCTAATTTTT TGTACTTTTT TTTTTTTTAA AGTAGAGATG AGGTTTCACC  
11651 ATGTTAGCCA GGATGGTCTC AATCTCCTGA CCTCATGATC CACCCACCTC  
11701 GGCCTCCCAA AGTGCTGGGA TTACAGGCGT GAGCCACCGT GCCC GGCTGT  
11751 AACACCTGGC TAATTTTTGT ATTTT TAGTA GAGATGGAT TTCACCATGT  
11801 TGGCCAGGAT GGTCTCGATC TCCTGACCTC GTGATCCGCC CGCCTCGGCT  
11851 TCCCAAAGTG CTGAGATTGC AGGCGTGAGC CACCGCGCCT GACCTTGTTG  
11901 GTGTTTTTAA GAGACAGGGT CTCACCCTGT CACCCAGGCT AGTATGCAGT  
11951 GGTGTGATCA TAGCCCACTG CGGCCTCAA TAGCTCCTAG GCTCAAGTGA  
12001 TTCTCCCACC TTAGCTTCCA GAGTACTGGG ACTACAGGTC ACACCTGGCC  
12051 CCCTCAACCT TCTGGACTTT TCACTACCC CATCACTCCC TACTTCTCCG  
12101 CCACAGAAGA CTGTCATTGG CTATCTTTGC AAGTAGTATT GAAGCCACTC  
12151 GGAGATTGTT GCTTTGTCTT TTTGCTCATG AAAGTTTGAA TTA CTGGTTC  
12201 TCCAGTCACA GGAAGTGGGG CTCCTTAGGC CAGCTCCATC TCACGTAGTG  
12251 TACTGATTAT GTTGAGCTTA TGGCACAGCT GAGAGGAGAG TCCAAACTTT  
12301 TTGAACACTT TTTGACTTCC AATAAGTGGT TCCACTATGG TTAAGAGCAG  
12351 GTTTGGTGGG CCGGGCGCGG TGGCTCATGC CTGTAATCC AGCACTTTGG  
12401 GAGGCCAAGG CAGGCGGATC ACCTGAGGTC AGGAGTTCGA GACCAGCCTG  
12451 ACCAACATGG TAAAACCTA TCTCAACTGG AAATACAAAA ATTAGCCCGG  
12501 TGTGGTGTTG TACACCTATA GTCCCAGCTA CTCGGAAGGC TGAGGCACAA  
12551 GAATCACTTG AATCTGGGAG GTGGAGGTTG CAGTGAACAG AGATCATGCC  
12601 ACTGCACTCC AGCCTGGGCA ACAAAGCAAG ACTTTGTCTC AAACAAACAA  
12651 TAAGAGCAGG TTTTGCGGCT AGATTTCTTG TATTGGAATC CTGGATCATC  
12701 CTCTCCTGTG ATCTTAGGTT CCCTCTGTGT CTGTTTGCTC ATCTGTAAAA  
12751 TGGGAGAAGA ATAGTACCCA TCTTATAGGT ATAGCTGTTA TGAGTATTAA  
12801 AAGAGTTAAT GAATAGAAAG CATTTAGAAT AGCGCCTGGC ACAGCAGAAT  
12851 GATCATTGTC ATTATTGTTC CAGTTGAACA ACACAGTGAA TTTTATCTGA  
12901 GCACCACACA ACTCTAGGTC AGTATAAGGG GTGATGTTTG GGATTTCTCT  
12951 GTAATCAGTT GAAAAAATCT TGTTCTGGCA TCTTCAAGCC ACTGGGGTCC  
13001 TATAGGTGCT TTTTCTAACA TTTCTGTTT TTTGTTTGTT TGTTTGTTTT  
13051 TTTGAGATGG AGTCTTGCTC TTGTTACCCA GGCTGGAGTG CAGTAGCACC  
13101 ATCTTGGCTC ACTGTGACCT CCACCTCCA GGTTCAGCG ATTCTCCTGC  
13151 CTCAGCCTCC CAAGTAGCTG GGATTACAGG CACCTGCCAC CATACCTGGC  
13201 TAATTTTTTT TTTTTTTTTT TTTTTTTTTG TATTTTTAGT AGAGATGGGG  
13251 TTTACCATG TTGACCAGGC TGGTCTTGAA CTCCTGACCT CATGATCTGC  
13301 CCACCTCGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACTGCACC  
13351 CGCCCTAGTT TGCTTTTTTA CCAATCACCT ATCTGAAAAA AAATGGAATG  
13401 CTA CTGGAGA GATTCATGTA CTTCTGAGAA CACTTTTAGC TCATTTTTTA  
13451 TAAGGCATCA ATATTAGATA GTTTTCTTGA TTAAAGAAAA AAAACACCA  
13501 CCCACTGCCT GCCTATATTT CTGGGTTGCA AATGATGGCG GTGGATGTGC  
13551 AGCCTCATCC GTGGCTAGAA GGCCAAATCC AAAGTCACCA GAGCTTGAGT  
13601 TTTTGTAGAG TTGAGATCTG TGTGTCAAAG GGAAGCCCT AGGGTGGTTC  
13651 TCTGCAGCAC CAAGAGCAGG GATTCATACC ATCATGTTCC TTTCTTTTTT  
13701 CTTTTCTCGT CTTTTCTTTC TTCCTTCTT TTTGTTCTCA TGAGTTCTCA  
13751 CTGTGTTGCC CAGGCTGGTC TTGAATATT GGCCTCAAGT GATCCTCCCG

FIGURE 3A-6

13801 CATTGGCCTC CCCAAGTGCT GGGATTACAC ACTCAGCCAT GTTCCTTTCT  
13851 TCAAGTACGG TATTGACCCT TTGGCCACAG GAGAACGTGC CCAGTTTTTC  
13901 TTAAAGACCA CGTGGGAACT CAGCAGCCCA TGATTGTAGG TTCCTTTTTTC  
13951 CCTCATAGAG TGGCCTTCAA GGGCAGGTTT TGTATCTG CGTTTCAGAG  
14001 ACCCAAAGGG ACACAGGCAT TTCTGCTCCT GGAATTTGC GGACTTTGAA  
14051 TCTTGAGCTC AGATTTTGGT CTCTGTTGGT TGCTTGTTTA TCTTCATCTC  
14101 TTGTCATTTT TGGAGCCTGC ATGCCTTCTC AGAGCAGCAG GTAAGTTGCT  
14151 TAGTTTTTTC ACATTGAAGC TGTGGCTGGG GGAAGGTAAC AGTGTCCCCT  
14201 CAGAACTCAT GGAGATGCCA GGCATAGTGG AGGCTGAGGC AGGAGGGTCA  
14251 CTTGAGGCTG GAGGATTGCT TGAGGCCAGC CTGGGCAACA TGGTGAGAGC  
14301 TCATCTCTAA AAAATTTTTT TAAAAATAAC TCATCAGGGG CTATTTCTTT  
14351 CATTGTATTT TCCTCTTCCT TTTGAACCCC TCTGCTGACT TGTTTCACTT  
14401 TCTTTTTTTC TGTTTGGTTT CTTTGAAGTC CTTTCTTCA TTATCATGTC  
14451 CTCATTCCCG TCCATCTTAG GTTTTTTCACT TCCTTGTTCC ACTCTCCCTA  
14501 ACCTGTTTCT GTGCCCTGTT TATGGCATGG CTCAGGATAT GAATTTTGAT  
14551 CTCCGTCTGA GATCTCCTTC AGGTATAGAA TCCAGACCA CCTGGTCTTT  
14601 TTGTTCTCTC ATTCCTCTGA TTTCTGTACA TTAAAGGATT CACTGCTTTA  
14651 GAAAACTTTT TTTTTTTTTC TTGTTTCTGG AGCCACCTCT CTCAGTAAAG  
14701 CCAGGCTTGG CAACTTATTA GGGACAGCAT TCTGGTTTCC CTGGTGACAG  
14751 GGTTTAAGCT GATTCTAGGC TGTGCTCTT AACCCTCAG GAATGCCATA  
14801 AGTATAGACC CTGTCTTGGG AGAGATCTGG AGAGATACTT GAGAATTTTG  
14851 GACACTGTAA TATTGAATTT GGTCTAATT GTGATCTAGA GACCCTCAGA  
14901 CTCTTTCAGG TGATGCACGA AGTCAAAATT CTGTTTCATAG TAACGTTAAC  
14951 ACAGTGTTGC TTTTTCATCT TCATTCCCTC ACCAGTATAC AGTGGCATTT  
15001 TCCAGAGGCT AAATGATGTG TGGTAACATC ACATTCTTCT GGCTAATGAA  
15051 ATGTGTAATT CTGTATTCTT GTGTTTTCTA TAATTTTTTAA GGTAAGTACTT  
15101 TAAGGTAATA ATATGGAAGT TTTTATTGAT GGACTCAGTT TGTCTTAGT  
15151 ACTTCTGTGC TCTTACTAGG TTTCTTCAGT TATAACTGCT ATCATCTTTT  
15201 TGTACACTTC ATTACTGTCT AATAAATCCT TATTTTGAAA TCCCAGCATT  
15251 TTCCTGGAAC CTTTGAGAAA ATATAAGAAG TAAGTACTAC TTGTAAAAC  
15301 TGCTTGTAAG AACTTTTGGG AAAACTCCTA ATTTTAAAAA TTTTATTGAC  
15351 AACTTATTTT AGCACTTTAT TCTAAAATAG AAAAAAATTT ATATTATTTT  
15401 TCTTATATGT AAGGGTGGAT TGTGCTTAA AAAAAGGGAG ATTAGAAGAC  
15451 TTGCTTTTTT AACCCATAGC TGCAACTTGT ATGTTAAAAA TACTGAAGTG  
15501 GACATACCAA CAAGTATAAA GGAGGACTTT AAAGAATCTG GGCAGAAGTG  
15551 TAAATAAGAA CTAAAAAAGG AAAAAAAGAA AAGAAATGAA AGTGTAAATGA  
15601 AAGCTACCTT CTCAGTTTCA TAAATGTTCA TAATGTACCT TACTGCGTCT  
15651 TATGCGACAG AACATTTTCA TGTAAGTATTA TGGTACCAGT TAAGTTGTGG  
15701 CATTCTTTCA AGATCATTTA GAGTTTAAAG AAAAAGGAAT TGCATATTTT  
15751 ATGCGTACGT ACTATGAGCT CTTTAAAGC CAAAATTTCT TCCAGTTTTT  
15801 AAAGTAGAAA TAAAAAAGTC ACTGAAGCCT CTATCTAACA GGATAAGTTG  
15851 CCACATTGCT TTGGCTGGAA AAGCCACAC AGAAACTGAG AGACGAATGA  
15901 AGTCTTGAAC AGCTGACATT CCTGAATGCC CACTGGATGA AAAGTCAGTA  
15951 AAATTCAAGG CAGTGCCGCT TTAATGTGTA CCAGGATTCA TTAAATTAAA  
16001 GATTTAGCCA GCGCGGTGG CTCATGCCTG TAATCCCAGC AGTTTGGGAG  
16051 ACCGAGGCAG GTGGATCACC TGAGGTCAGG AGTTTGAGAC CAGCCTGGCC

FIGURE 3A-7

16101 AACATGGTGA AACTCCTTCT CTAATAAAAA TACAAAAAATT AGCCAGGCGT  
16151 GGTGGCGCAT GCCTGTAATC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA  
16201 TCGTTTGAAC CCAAGAGATG GAGGTTGCAG TGAGCCGAGA TCGTGCCATT  
16251 GCACTCCAGC CTGGGCGACA AGAGCGAAAC TAAAAAATAA AAAAAAGATG  
16301 TAGCTGCACA CATGAAGACC AAGTTAATAT CTTATTTACA GAATTTTACT  
16351 TTCACCTTAC AAATGAGCAA ATCTATAGAT GTGGCTCGAC TTGCTGTATC  
16401 AGCACCAACT GCTCATCAAA GAATAATTTA TTTTATGTGA ATGCTCAGCA  
16451 GCAGATACAA ATGGTGATAA ATATTCAAAG GGTTGAATAA CTTCTGAAT  
16501 CTCATGACTT ATCCTGGAAC AACTTTATTT CCATTTGCAC CTTGGTGCA  
16551 GAAGCAGTGG TGGAGAAAAC TGCTGACGCC GTAACATGGA TCAAGGAAGT  
16601 GGCACTAAGC TCTACTAGTG GTCATTGTCA TGGTCTTCTT TCCCACCACA  
16651 AACTTGTGGT TGAAAAATAA AAGCCATTTT TACTTGAGAA TGTCTTGAAT  
16701 GAAGGATTAA AGACTATCAT TTTTTTTATT TACTTATTTA TTTATTTATT  
16751 TATTTTAATT TTTATCTATT TATTTTTTTG AAACAGAGTC TCACTCTGTC  
16801 TCCTAGGCTG AAGTGCAATG GCGTGATCTG TGCTCACTGC CACCTCTGCC  
16851 TCCTGGGTTT AAGTGATTCT CCTGCCTCAG CCTCCCAAGT TGCTGGGATT  
16901 ACAGGCACCT GCCACCACGC CTGGCTAATT TTTGTATTTT TAGTAGAGAC  
16951 AGGGTTTCGC CACGTTGGCC GGGCTGGTCT GGAATTCCTG ACCTCAGGTG  
17001 ATCCACCTGC CTCGGCCTCC CAAAGTGCTG GGATTACAGG CATGAGCCAC  
17051 CATGCCTGGC CAAGACTATT AATTCTGTGT GTGTGTGTGT GTGTGTGTGT  
17101 GTGTGTGTGT GTGAGGTCTC ACTGTGTGAC TTAGGCTGGA GTGCATTGGT  
17151 GCAACCTCCG CCCACTGCAA CCTCTGCCTC CCGGGTTCAA GTGTTTTCTC  
17201 ACCTCAGCAT CCCCAGTAGC TGGTACTACA GTGGGGATAC TCCACCCCAG  
17251 GAGTGAAGCA TATAACCCAG TTCCNNNNNN NNNNNNNNNN NNNNNNNNNN  
17301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
18001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
18051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
18101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
18151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
18201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
18251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
18301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
18351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

FIGURE 3A-8



18401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNCCTC	CCAAAAAGGT	AGGGTTTCAG
19801	GTTTGAGCCC	CTCGCCACCC	GTCCTGGTTT	TTAATTTTTC	TCAATTTTTT
19851	CCCCATTTTA	AAATTTTCCA	AGGGTTTTTT	TTTTTTTTTT	TTTTTTTTTT
19901	TTTTTTTTTG	AGACAAAGTC	TCTCTCGCTC	TCTCGCTCTC	TCACTCTCTC
19951	GCCCAGGCTG	GAGTGCAGTG	GCGCCATCTC	GGCTCACTGC	AAGCTCTGCC
20001	TCCCGGGTTC	ACGCCATTCT	CCTGCCTCAG	CCTCCCGAGT	AGCTGGGAGG
20051	GACTACAGGC	GCCCCCACC	ATGCCCGGCT	AATTTTTTGT	ATTTTTATTA
20101	GAGATGGGGT	TTCACCGTGT	TAGCCAGGAT	GGTCTCGATC	TCCTGACCTC
20151	ATGATCCGCC	CGCCTCGGCC	TCCCAAAGTG	CTGGGATTGC	AGGCATGAGC
20201	CACCACGCCC	GGCCTAAATT	TTTCAGTTTT	TATACTCATT	TCCTTTTTGT
20251	TCGTTTTCTT	TCTTTAATTT	GTTAGTATTT	GTTGTTTTTT	GAGACAGCCT
20301	CACTTTATCA	CCCAGGGTGG	AGTGTGGTGG	CACGATGTTG	GCTCACTGCA
20351	ACTTCCACCT	CCCAGGTTCA	AGCAGTTCTC	CTGCCTCTGC	CTTCCCAGTA
20401	GCTGGGATTA	TAGGCACTTG	CCACCAAGTG	ATTTTTGCAT	TTAGTAGAG
20451	ACGGGGTTTC	TCCATGTTGG	TCAGGCTGGT	CTCCATGTTG	GTCAGGCTGG
20501	TCTCGAACTC	CTTACCTCAG	GTGATCTGCC	TGCCTTGGCC	TCCCAAAGTG
20551	CTGGGATTAC	AGGCATGAGC	CACCGCCCCA	GCCTGTTTTT	TGGTCAGCTG
20601	TTTTGTTTTG	ATTGCATTAT	AAGATTAGTT	CATCAGGTAG	ACTTCCTTTG
20651	GTATATATTT	AGTTGTGGTT	TGGAAAATAA	GTTTTTTATT	AAAAATAAGT

FIGURE 3A-9

20701 CATTATGTT TACATGTAAT GAGTTTACTC ATGTTCTGTT AAATGAATTG  
20751 ATACATATTT AAATTTTTCC TCACTTGAAT TTCTAATATA GTAAATACTG  
20801 ATAGATAAAA TTCATATAAA CAAAAGCTTC TGGGTGTTCA GTTATTTTTTC  
20851 AAAATGCAAA GAGTCCTGAA ACCAAAAACT GTAAGAATCA TGGTTGTAGA  
20901 CAAAACCTGG TTTGGTTCTC CATGACTTTG GTTGATACAT TTTTTTTTTA  
20951 TTTTTTTATT TTTTGAGACA AGTTCTCATT CTGTCACCCG GGTTAGAGTG  
21001 GAATGGCATG ATCTCGGCTC ATTGCAGTCT CAACCTCCCA GGCTCAAGCA  
21051 ATCCTCTCAT CTCAGCCTCC CAGAGTGCTG GGATTATAGA CATGAGCCAT  
21101 TGTGCCTGGC TATATTATCA TCGTTATTAT TGTTTTGTTT TGTTTTTTGA  
21151 GATGGAGTTT TGCTTTGTCA CCCAGGGTGG AGTGCAGTGG CACCATCTCA  
21201 GCTCACTACA ACCTCTGCCT CCTGGGATCA AGCGATTCTT GTGCCTCAGC  
21251 CTCCCAACTA GCTGGGATTA CAGGTGCACA GCACCACACT TGGCTCATTT  
21301 TTGTATTTTT AGTAGAGACA GGGTTTTGCC ATGTTGGCTA GGCTCCTGGC  
21351 TTCAATTGAT CTGCCTGCCT CGGCCTCCCA AAGTGCTAGG ATTACGGGCA  
21401 TGAGCCACTG TGCCTGGCCC TGTAATATAA TTTTACATGA GTTAATAGTG  
21451 TAACATTTTC TCAGTTGTAA TTTTTTTTTT TGAGACAGTG TCTCACTCTA  
21501 TCACCCAGGC TGGAGTGCAA TGGCACGATC TCCACTCCCT GCAACCTCCC  
21551 AGGTTCAAGT GATTCTCCTG CCTCAGCCTC TTGAGTAGGT GGGATTACAG  
21601 GCATGCGCCA CCACACCCGG CTAATTTTGT TACTTTTAGT AGAGATAGGG  
21651 TTTTCACCAT GTTGTTGAGG CTGGTCTCGA ACTCCTGACC TCGTGATCCA  
21701 CCTGCCTCTG CCTCCTAAAG TGCTGGGATT ACAGGCCTGA GCCACTGTGC  
21751 CTGGCCAGTT TTAATTTTAA TACAATAAAT ATCAGTAGCT ATCACCACCA  
21801 TGAAGAAAGC CATTTGACGT CATCAGTAAG AGTAAAGGGA TTCCAGACAG  
21851 TGTGAGAACT CTTTTGTAAA CAGAGATAGG ACTGATAATC CCTGTCCTCG  
21901 ATTGGTTGAT TACTTGCTAT GACCTCATAA TGAGCCTCTG TTTTGCAATT  
21951 TCTGGGGCCC TGGCTGGGCC TCAGGAAGGC ACTTGCTGTC TTGGTTTTCA  
22001 GTTGTCTAG CTGAGGAAGC TGGTTCTCAG TGACCTGATG GACCTTGGCC  
22051 AAAGTTGGCT CATTTCTCCT TTTGAATACA TAGCATTACT TTATGTTTTT  
22101 TTATTCCATT AAAAAGATCA TTTGGCTTAC TTGGATTTTA TTATGAGGTT  
22151 TGTGTTTTAT TATGAGGTAG GTTTGTGTTT TTTTGTTTTT TTTTAACTT  
22201 ATATGTTGGC TATTGGTCAG TTCCAAATTT GAAAACCTGCA ACGCTTACAC  
22251 AGCTTCTATC CTTGAAGAAC CTTGGTGCCT ACAATAGCTG AGAGCTGGTA  
22301 GGCTGCAGTC ACTAAGGCCA GACACTCAAT AGTCTATTCC CTGGGTGGCT  
22351 TGAGACCTGA CATACTTTGT TTCTTTTTGT TTCTTTTCCT TTTGTACTTG  
22401 ACTCTTTTTA ACCTGTTTAT TTCTTTTTTT TTTTTTCCC CGAGAAGGGA  
22451 GTCCTGCTCT GTCACGCAGG CTGGAGTGCA GTGGCACGAT CTCGGCCAC  
22501 GGCAACCCTC CGCCTCACAG GTTCAAGCAA TTCTCCTGCC TCAGCCTCCT  
22551 GAGTAGCTGG GATTGCAGGT GCCCGCCAGT ATACCCGGTT AATTTTTGTA  
22601 TTTTATAGTAG AGAAAGGGTT TCACCATGTT GGCCAGGCTG GTCTTGAATT  
22651 CCTGACCTCG TGATCCACCC ACCTTGGCCT CCCAAAGTAC TAGGATTACA  
22701 GGCACAAGCC CATGCCTGGG CTAACCCCTA TTTCTATCTT TCTTTTTTTT  
22751 TTTCGAGACA GAGTCCCACT CTGTCGCCCC GGCTGGAGTG CGGTGGCCGG  
22801 ATCTCAGCTC ACTGCAGCCT CCACCTCCCA GATTCAAGCA AATCTCCTGC  
22851 CTCGGCCTCC CGAGTAGCTG GAACTACGGG TGCGTGCCAC CATGCCCGGC  
22901 TTATTTTTGT ATTTTTAGTA GAGACAGGAT TTTGCCATGA TGGCCAGGCT  
22951 GGTCTTCAAC TCTTGACCTG GTGATCCACC TGCCGTGGCC TCCTAAAGTA

FIGURE 3A-10

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23001 CTGGGATGAC AGTCATGAGC CACCACATCC GGCCTCTAAC CCTTGTTTCT
23051 TAATGAAACA TACCTGTAAA CCCCACTGTT ATGTAGGTAT ACTTTATTTT
23101 TCCTGTAAGA GGTAGGTTTA TTTGGAGTGT TTGTAGCAGT GTGTGAACTT
23151 TGTATTTCTT TGACAAGTCC TTAAGTGACA GGGAAAATTG TAGTAGTATA
23201 TAATCTGTAA ACTACCCTGT AATTCTCAAC TTTGTTCTTT TGCATATACT
23251 CATTCTCCAA TTTCCATAGC ACCTCTAACT TTTAACAGCT TCCCTAAGTC
23301 CTACAAATAA TAGACCTTGG GCCTCCTCTA ATAGTCACTT TGACCAACTT
23351 TAAGCAAATC TTTTAAAACT CATGTGCGCT GGGTGCAGTG GCTCACTCCT
23401 GTAATCCAG CACTTTGGGA GGCTGAGGCG GGTGGATCAC GAGGTCAGGA
23451 GATCGAGACC ATCCTGGCCA ACATGGTGAA ACCCCGTCTC TACTAAAAAT
23501 ACAAAAATTA GCCGGGCGTG GTGGCGTGCG CCTGTAGTCC CAGCTACTTG
23551 GGAGGCTAAG GCAGGAGAAT TGCTTGAACC CAGGAGGGGG AGGCTACAGT
23601 GAGCCGAGAT CATGCCACTG CACTGTAGCC TGGGTGACAG AGACTCCCTC
23651 TCAAAAAAAA AAAAATAAAT AGAAATAAAA AAGCCAGGCA CAGTGGCCCA
23701 CATCTGTAAT CCCAGCACTT TGGGAGGCCA GGGCGGGTGG ATCAGGAGGT
23751 CAGGAGTTCG AGACCAGCCT GGCCAATATG GTGAAACCCC GTCTCTACTT
23801 AAAATACAAA AAATTAGCTG GGTATGGTGG CGCGTGCCTA TAGTTCCAGC
23851 TCTTCAGGAG GCTGAGGCAG GAGAATCACT TGAACCCAGG AGGCGGTGGT
23901 TGCAGTGAGC ATAGATCACG CCACTGCACT CCAGCCTCGG TGACCGAGTG
23951 AGACTCCATC TCAATGAAAA AAAAAAACA AAACAAAAAC TCATGTCATT
24001 TGCTCAGAAT CACATCTCAT TGGAAATCATT TTTTAAAC TGTTTAATCA
24051 AGTGCTCAAC ATATCAATTC GTGTCTACAT AGAGGATCAT AGCTCCATTT
24101 CCCATCACTC AGCAAGTCCC ATAATCTGCT TTTTCCACAA AGCGTATTTT
24151 TTTTCAGATT TACATGTGGC ATGCATTTCA GTTCCAGAAT TGAACCTAAT
24201 GTGCTATTTT CTCTCTTCGG CTACTGGTCT GTGTGGAAGA TAAGGAACTT
24251 TAATTTTCGG TTGGGTGCAG TGGCTCACGC GGGTAATCCC AGCACTTAGG
24301 GAGGCTAAGG CGGGCGGATC ACGAGGTCAG GAGTTCAAGA CCAGCCTGGC
24351 CAAGATGGTG AAACCCCATC TCTACTAAAA ATACAAAAAA CGTAGCCAGG
24401 CGTGGTGGTG GGCGTCTGTA ATCCCAGCTA CTCTGGAGGC TGAGGCAGAG
24451 AATTGCTTGA CCCCAGGAGG TGGAGGTTGC AGTGAGCTGA GATCGCACCA
24501 CTGCACTCCT GCCTGGGCGA CAGAGCGAGA CTCCGTCTCA GAAAAAATA
24551 ACAAGAATTT TAATTTCAAA TATTTGTTTA CTGTATTAGT TAAGGCAACG
24601 GCTTAGTAAT GGCACCTCCT GGATGGCCCT GTAAGCGCAT TAATCTGGTC
24651 CAAGTCATTG GGAAACTCAG CCTTAAAGGG AATGGACTGA GTGGTTGAAG
24701 AGTAGGCAGG GTCTCCTCAT TTTTGCATGG TTTGCCTCTG AGGCTGTGTA
24751 TCTTTAGCTA CAGACAGAAT AGCTAACATT TATTGAGCCC TACTCTGTCT
24801 GCAAGCACTT GTTTAGTTGT TTTACATTCA TTAATCATT TACTCTTTTT
24851 TTTTTTTTTT TTTGAGACAG AGTCTCGCTC TTGTTGTCCA GGCTAGAGTG
24901 CAACGGCACA GACCTTGGCT CACTGCAACC TCCGCCTCCC GGGTTCAAGC
24951 AATTCTCCTG CCTCAGCCTC CCAAGTAGCT GGGATTATAA GTATCTGCCA
25001 CCATGCCTGG CTAATTTCTT TCTTTCTTTC TTTTTTTTTT TTTTGTAGAC
25051 GGTGTTTCGC TCTTGTTGCT CAGGCTAGAG TGCAGTGGCA CTGTCTTGGC
25101 TCACTGCAGT CTCCGCCTCC TGGGTTCAAG CAATTCTCCT GCCTCTGCCT
25151 CCCGAGTAGC TGGGATTGCA GGTATCCGCC ACCATGCCCC GCTAATATTT
25201 TGTATTTCTA GTAGAGATGC GGTTTTACCG TGTTGGCCAG GCTGGTCTCA
25251 AACTCCGGAC ATCAGGTGAT CCACCCATCT CAGCTTCCCA AAGTGCTGGG

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FIGURE 3A-11

25301 ATTACAGGCA TGAGCCACCA TGCCTGGCTT CATTTATTCT TTGTAAGTTA  
25351 GTAGATCTCA CTGTTTTACA GGTGAGGAAA TAGAGGCCCA GAAATGTTGA  
25401 ATAAC TTGTT TAAGGCTACA AACCCAGGTG GTCCAGAGTA TGTCAATTGTC  
25451 AGAACCAGCT TTTCTTGGTT GTGAAGAATC CTTTGTCCCT GGCTTCAGTT  
25501 GTGTCCAGGC AGTAGAAGAT AGTTTCCTTA GGATTAGCTC CCAGTCAGTG  
25551 TGAGGCAGAT GTCTTGACGC GGAATTTAGA GTCACAAATG GCCTCCTCTG  
25601 CCTCCAGTTG TTTCTTTTGT CCTTGGTGGC CATTGGTAAA TGTGGCCGAA  
25651 ATGGTGTGGA TGGAGTGGGA GCAGCTTTCT GGGCTCACCT CCCTACTATT  
25701 GAGGGCTCTA CGCAAGAGCT ATGGGAGACC TTTTAAAGAA ACCCTCTTTA  
25751 ACCCCAGCTT CTGATTCACA TCTTTATCTT TTCCCATCTT CCGGAATTTCT  
25801 AAGAACCCCT TTAGAAAAAC CAAAGCCCCG AGTCCTAAAA TTGATAACCA  
25851 GCAATTAAGT ACCTTAAAGT GTAGGGCATG ATGGATTTCT AGGTTTGACT  
25901 ATCCTGCTTT GTGGCACCCA TGAAATGTTG GGATTCTAGA ACTCTTTCTT  
25951 TGTAAGCACC CCACTCCCCA CCAAAAAAAA CCCCCTAAA CATAAGAAGC  
26001 TTTTGTCTGT GGATCTTAAC TGTGTATATT TTGTCTCTAG GAAGCAAACCT  
26051 CAGATTCTCT CTTACAACCG TCTGTGTGCC ACTTGACACAC ACACAGGCAC  
26101 AGAGCTACTT GCTTGTAGCC TTGACTGCCA GCAGCCCTGA ACACCGTAGC  
26151 TGGTGGTGCC AGGCCTTGTG TGTGTTTAGG ACTTGCCAGT TCAGTCCTGG  
26201 GAGCTGAACCT CTGGACATCC TGCTGTGTGT CTCTTTATCC CATCGCTGGT  
26251 GTAATTTATG CCACTACTTC CTGTTTGCAT TTGCTCAGTC TCTCCTTTGG  
26301 TTTGCTTCTC TCTGCTGAAG CCGGTCCCCA TAGCTGTGCA CATGGCTAGC  
26351 TATGGGGACT AGGCATCTAG ATATTCTAGA CATCTGCAGT TGTTTCTTAG  
26401 TGGGAATGGT TGCTTTATGT CTCTCTACAG AATTTTAGTT GAACTTGAGT  
26451 GTATGATTTA ATTTACTTGC TTGTCTAACT TCGGCAAGGG TGCCTTTTAT  
26501 TTTAAGATGC CAGCATGGGG TGAGAGTAAA GGGGTGAACCT ATTGCCCTCC  
26551 CCCACCCCCC CACCCCCCAC CCCCCCACTT TTTTTTNNNN NNNNNNNNNN  
26601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
26651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
26701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
26751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
26801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
26851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
26901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
26951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

FIGURE 3A-12

27601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
27951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
28001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
28051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
28101 NNNNNNNNNN NNNNNNNNTA TTAAATAAAT AAATAAGATT TACTTATCCA  
28151 AAAGCACAAT TATGTGCTT TTTCTTTTC TTTTGAGACG AGAGTCTGAC  
28201 TCTGTTGCC AGGCTGCTGT AGTACAGTGA CGCAGTCTCG GCCTTGACCT  
28251 CCCAGGCTCA AGCAATCCTC CCACCTCAGC CTCCCAAGTA GCTGGGACTA  
28301 CAGGCATGTG CCACTATGCC TGGCTAATTT TTTGCACTTT TTGTAGAGAT  
28351 GGGGTTTCGT CATGTTGCCC AGGCTGGCCT GGAACCTCTG GCGTCAAGCA  
28401 ACCTACCTGC CTTGCGCTCC CAGAGTGCTG GGATTACAGG CAGTCGCCAT  
28451 TGTATCCAGC CCAGTTATGT AGTTATGTGC CATTTCTAAA CTACTTTAGA  
28501 ACCCATCTCT TTGGTGTTG TTTGTTTGAG ACAGAGTCTC ACTCTGTCAC  
28551 CTCAGCTGGA GTGCAGTGGT GTGATCTCAG CTCACTGCAG CCTCGGCCCC  
28601 CAAGGTTCAA GCGACCCTCC CACCTCAGCC TCCCAAGTAG CTGGGACCAC  
28651 AGGTGCTCTT TTTGTTAAGA GTGGAAAAGC CAAGGTCCAT GTACTTTTTT  
28701 TGAGAAAGAC AGCCTGTTGG CTTTCTTCAG AGTGGTTCTG CCCCTTCCCG  
28751 TACCCCATCT CCAACACATT TTTATCTCTC AACAGAGGTA GCTGCTATTC  
28801 ACTCAGGTGT TCTTTAATGC TGTGGCCACG GCTTCCTTGG AGAGTGTGGC  
28851 AGTGCTTTCC TTGCTAATGA AAAGGCTGTC ATAATGGGTT AGGTCCATAG  
28901 GGGCTCTGCC CTTCTGTACT TGTATTCCA GGGAGAAAAA TCTCTACCTT  
28951 AATTACCGAC ATCTCATGCT GGCAGAGAGG TGTGGTTGCT AATTGATTAG  
29001 ATGACAGTCC TTTTCATTGA TGTGGCACTG TTGGGGTGGT TTTGTTGTGC  
29051 TTTTCAAGT AAACAGATAG ATTTGGGCCA GGTAAGTTGA TTTTGGAGAG  
29101 ATGAAGTTCT GTGTAGGGAT TTCCCTTTAT TAAGCTCATG TCTTTAGTGC  
29151 CACTTTTGTG TCCTGATTTT CTAACCTGAT AGTAAGAAGT ACTAAGTTGG  
29201 CTTGTCTTGC TATTTTGGTG TGGGTGGTGA ATAATGTCTC TTCTACCCTG  
29251 CTCTCTGGTG CGTTCCTGTT CTGTTTGGTA GCACCACATT CCTCTATTTC  
29301 GTTTGGTTTT CATTCCCTCT TTCTCTCTTG TAATGGTTGG ACCCTATTCT  
29351 GAAATATATA TTTTAAGATA GTGTTACTTT GGGTGGTCGA GGCGGGCAGA  
29401 TCACCTGAGG CCAGGAGTTC GACACCAGCC TGGTCAACAT GATGAAACCC  
29451 TGTCTCTACT AAAAATACCA AAATTAGCCA GCGTGGTGG TGTGCATCTG  
29501 TAATCCCAGC TACTCGGGAG ACTGAGGCAC GAGAATTGCT TGAACCCAGA  
29551 AGGCAGAGGT TGCAGTGAGC AGAGATTGTG CCACTTTACT CCAGCCTGGG  
29601 CAATAAGCA AGACTCAGTC TCAAAAAAAA AAAAAAAAAA AGTAGTGTTC  
29651 AAAAGCAAAC ACCCTGCCTT TTTTGAAACC ACAGAAACTG CTTGTGAAAC  
29701 AGCCGATAGG GCAGGCTGCC AAATACAGAC TGTTAAAACC AATCTCTTAA  
29751 TGACAAAATG TCAAAACACTG ATGTTAAACC TTCATTATGA CTGTGGTGTG  
29801 AGGATTTTTT TCAATAAGAA ATGTTTAGGT GCTGAACTCC CAGTTTCACA  
29851 TTCAGAATGC TTCTATTATC AAATTCCTCT TGGTACATCA TTTCCGAGAG

FIGURE 3A-13

29901 GCTTGTGTAG CTAATCCACT ATCTACTGTA CAGGAAAGAT TTAAATAAA  
29951 CCTATTCCCA TTCATCCTCA TCTGTGTTTT TTTGTTTTTT GTTTTAATTT  
30001 CAAGAAGTAA TTTTCTTTTG AGGTGATTG GACCAACCGT CTCACTAGCT  
30051 TTTCCCATTT AAGATAGGAG AACTAGATTC AGAATTGTGT CTTTTTCCTA  
30101 ACAGAAGACT GGGGCCTTAA TCTTTACCCC CCAGGCTCTG ATTAAGTAC  
30151 TTTTCTTTTT TTAGATGGCA TAGAATCTTC TGTCTGTCTA GAGAATTTTG  
30201 TTTCTTGCCA GGCAGTGTCA GGAATTAGTA TTCATTCTCCTC CTGCTATCT  
30251 TCCTGAAGAG CTGTGAACCT GCTGGTAGCC TGATGGATAA GGGTACAGTT  
30301 GTTTGTTTAT TTATTGAGAC AGGGTCTCAT TCTCTACCCC AGGCTGGAGT  
30351 GCAGTGGCAT GATCTTGGCT CACTGCAACC TCCGCCTCTC AGGCTCAAGC  
30401 TATCCCCCAA CCTTAGCCTC CTGAGTAGCT GGGACCACAG TCATGTGCCA  
30451 CAACACCCAG CAAATGTTTT GCGTTTTTTG TAGAGACAGG GTTTCCCAT  
30501 GTTGCCTTTG CTGGTCTTGA ACTCCTGGGC TCAAGTGATC CGCCTGCCTC  
30551 AGCCTCCTGA AGTGCTGGGA TACCAGGTGT GAGCTACCAC AGTTGGCCAA  
30601 GGTATAGTTT TATGAGCTGA GCTATAGAAC TGGTTGAATG GGAATTAGGG  
30651 AAAACAGACA ACCAATAATT GGAAGTAAA GGAAAAATAT ATAAGTGTGC  
30701 CTCCTTGGTC ACAGCTAGCC TTGTGACATT GGGGTTTTGG ATATAGAAGT  
30751 TCAGGAATCC CTTCCACCTC CTTCCCAAGA GAATTTCTTC TGTTGGTGT  
30801 GTAAGGGGCT TTTTCCAAC TCAATTTCCAT TACCAAGAGT CTTGAGTGGC  
30851 TTTATTTTCA ACTTGGGTTT TTTAAGCGCT TCTCATGTCA CCTTTGTTTG  
30901 TGTACTGGGC CTGTCTCAAG TTTCCAGAGG GAGATGAAAG ACAAGAAAAG  
30951 CTAAATGACT GGTTCTTCAG TGAGTTTCCC AGAGTGGCTT CTTCTCATTC  
31001 CAGCACTGCC TAACTCTCAC CATGGCTGAC GCCGTGGGCA GGCATCCGCA  
31051 TTCATGGAAA GCCAGGTCCT AGCTGGAAGT GACACAGGGA TCTTCAGATC  
31101 TCTCTTAGCC CACTGTTCTC CTGAAAAAAA AACAAAAGCC ATAGACAGTA  
31151 AATTGGGGGA ATAGGCTGAC CATAACTTCA GTTCGTGGAT TTGGGTCCCA  
31201 CACTGGATTG TGTGATTTGT GCTTATCTCC TACTAGATTG TTACCTTCTT  
31251 TGAAGGCTGG ACTGTATCTT ATCCTTCTCT GTATCACTTC GGACACCCAG  
31301 AAAGTGTGG AGTACTTTGC ACATGGTCAC CTCTTAATGA ATTATTTGTG  
31351 AAACAAAAT TTTTTTAAAT TGTAACATGA GGCTGGGTGT GGTTGCTTAG  
31401 GCCTGTAATC CCCGCACTTT GGGAGGTAGA AGTGGGCAGA TTGCTTGAGT  
31451 CCAGGAGTTT GAGAACAGCC TGGGCAACAT AGCGAAACCC TGTCTCTATA  
31501 AAAAATAGAA AAGTTAGCTG GGTGTGGTGG TGCGGGCCTG TAGTCCCAGC  
31551 TCCTTGGGAG GCAGAGGTGG GAGGATTGCT TGAGACCTTG TCTCAAAAAA  
31601 ATAAAAAAA ATTACTTAAA AAAATCGTAA CATGGGTATT CTCCATTACA  
31651 GTTACCCTTA GGAAGTGTG TCCATATTGA TTTGTAAGTC TGATATCAGT  
31701 CTATCTGATT CTTTGGCTGT GTAAGTCACA AGTCTTAACC AGTATCTTAA  
31751 GTAGGTGTGG TAATGACTAC AGAGAAGTGC TTTTTCAGGA TGAGAAGATG  
31801 AGGGAGAAAA TTTACACCAT TGCTGGATTG TGTTAAGAAC TCGGAGAGGA  
31851 AACCACAGGG AGGATGCACT GCTGAGGAAA TCGTCTGGCT TCCTGGAGTG  
31901 GGGACCAGAG CCAGAGAGCC AAGCCCTCCT GGCTTTGCTG AGTTCTGTCC  
31951 TTGCCCCCTGA CACCAACGTG TCTGCCTGCT TTGTTGCTCC TGGTTACAGT  
32001 GGGCTCAGTC TTGCCTCTTT TTTGATGGGT GGGCAGAGGA AACTAGTGT  
32051 TGGGAATATT GTCCAGCGTT GGAGAGATCA TGTGGTCTGT CAGAAGGCTG  
32101 GAGTTATTTA TAGTGGGAGA AAAGCCCAGG AGCATGGCAC GGAAGAAGT  
32151 GATTTACAC CAGCTCAGCG CCTGATGATG GTGAGGACCC AGATTTTCTC

FIGURE 3A-14

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32201 TTGAGCATCT CAGAGCAGAT CAGTCGCTTT TCCTGATTGA CCCATGAACT
32251 GTGAGACTAG GGACCATGTT TTCCGAGGCC ACTGTGAGTG AGGGAAGAGT
32301 GAGAAGGATG ACCATTTTCT TCTTCCTTGA TTCTGGTCTT TGTGATGTGT
32351 GGTATGAAAG TGTACCTCTGA CTTTTGAATC TCCTTTTATT GAACTGGTGA
32401 AGAAGGCACC AGCTGTGTGG GGTGGTGGAA ATAAGGACCT GTTAAACTGG
32451 TCTGCCTGTA TCTGCCTCCC TGCTCCCCC TCACCCACC CACCCACC
32501 CTGGGCAGGG AGGCTGAAAC TGCTGCTTGC TAGGCTTTGC CAACTCAGTT
32551 TCTCTTCATG GATTACCTGC TCGCGGCAGG CAGGCAGGCA GCTCCCCACC
32601 TGGAAGCCTG CAGACTCGCC GAGCTGAGAG AATCATGCTG CAGGTGGGGG
32651 CAAGTGCTAG GAACTAGGTG TGCCACTTAC CTTAACAGGA GCTGTGCCTA
32701 GTCCGGGCTG CTCAAATAA GGCTGCAGAG CCCTGGGGCC TGTTGGAAAT
32751 AGACTGTGCC TTTCCCTGCG CCTTGTTGGC ACATTTTAT GGTATGTGGA
32801 GAGTCTGGGA GGGGCCGGGA GCTTGTAAT TGTGAGTAA TGAAGTCTAG
32851 GGAGGGAGAT GATCCTTCTT GAGGGCACCC TGAGTTCAGG GTTGTCTGT
32901 TTCTGAGGTG TGCTACTGCT TAGTACCCTG ATTTCTGGAG TTGTCTACCT
32951 AGGTTGCTTT TAATTTTTC AGCCTTAGGT GGAAGAGATT TTCCATCTTG
33001 GTGTTTAGGC ATGTTAGGTG AGGTTTACTT CCGGAGCCAG ACTTTTAGGC
33051 AGGTTGTCTT GACATAAGTC AAGGTCAGGA AGCGATCTT AGGACATGCA
33101 GACGATGCCC ACTTCCTGCT GTGGTCTTGA AGAGGGCTGG AAGGCTTGTG
33151 AGCACAGAGG CACTGAGGGC TGTCGCATCC ATACAGGAAG AACTCAGGG
33201 CTCGTCTCCG GTGCCTCATT TTATAAGCAT GGAAACAAAA GTCCCAGGAG
33251 GGTGAATGAC TTGCCCAAGG TGACATAAAT TGTTTGCGCA GAGCTGGGTC
33301 TAGAATGGAT CTTATGCCCT TGGCAGCGTG CCCCATTGC CATCACTTCA
33351 GAGGGGCTGG CTGCAGCCCT CAACGGCAGA AGGCAAGCTG GGAAAGGACA
33401 AGTGGAAGGG TAGCAGGCCC CAATTCTGCA CACTGGAGAG CACCTCTGAA
33451 ATCCTGCCGG AGACTATGCC CATAGAGGTG CCAGAGGCCC TAGGGAATGA
33501 TGATTTATTT TGTATTTTGT ATTTTGTGG AGACAGGGTC TTACAATATT
33551 GCCCAGGCTG GTCTCAAATC CTAGGCTCAA GTGATCCTCC CACCTGGGTT
33601 CCCAGAGTGT TGGGATTGCA GACATGAGCC GTGGCGCCCG GCTGGGAATG
33651 ATTTAAAAGT CGGCACCAGC ATTCTAGCCC TGACCCAGGC TAAAAGGGGT
33701 CACATGGAGC AGAGCTGTGC AAAGAGCTTT TGGGTGAGGA GTCACCTCCA
33751 GAAAAGCGAG AAGACTCTGA CCCCAGACT TCCCGTGGTG AGTTAGGAAA
33801 GCATTTCTGG AGAGCCTGTT AGGTGCCAGG CACTGTGGCT GGGCACTGAA
33851 GACACGAAGT GATTTAGTCT TGGAAATTCC CTTATGCTGC TCTCAGTCTG
33901 TGTAATAGTG AACAAGACAG CCAACAAGAG TTGTGAAGGA GGCCGTTTCA
33951 CAAGCAATGA AGTGCTAGTG CAGGAAGGCC CGAGCTGGGA AATGTCCGGA
34001 GAGACCCTGT GAAGTGATGC AGGGATCAGG AAAGCTTCCT GGTGGAAGCA
34051 ATGTCTGAGC TGAGGCTCAC CACAAAGAGG AATGGGAGTG ACTGCTAGAG
34101 GGAAAGTGTT CCAGGCAGTG GAAAGCTGTG GCCAAGACCT GGGGGGTTCT
34151 GAGAGGCCAT TGTACATTTG AAGACAGGTG GCTGGAACCC AGAGTGAGAC
34201 TCTAGGAAGG GAAGAGAGTT AGTCTGGAGC TGCAGGCAGG GAAGGGGAGA
34251 CAGCCAGCTC ATAATACAGT GTGGGCAAAA ATCCAGAAAC CATGTGGATC
34301 TAATTTGATA TCAATTTTAC ATGTATATGT GTATATACCT ACACACACAT
34351 ACATAAAATC AGTTATGTTT GTGTGTGTGT ATATGCATAT TTGTGTGTGT
34401 GTGTACGTGC GTGCATACAG AAAGTTGTTT TTTTAAGGCA TGCTTTAAAT
34451 ACGAAGCCAT CACTTCCTTT TCCCAGTCCT GGGTGCTTT TGAGATGAGT

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FIGURE 3A-15

34501 GTTGGTGCTC CCCCCACCGC CATGTGCCAT CTTCTGGAGT AAGAGGGAGT  
34551 GCTTTCACTG TGTGCAGGTG TGGCTAAAGA GTATTCAGTG TGTGCAGGTG  
34601 TGGGTGAAGA GTATTCACCG TGTGCAGGTG TGGCTGAAGA GTATTCACCG  
34651 TGTGCAGGTG TGGCTGAAGA GTATTCAGTG TGTGCAGGTG TGGCTGAAGA  
34701 GTATTCAGTG TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCACGTG  
34751 TGGCTGAAGA GTATTCAGTG TGTGCAGGTG TGGGTGAAGA GTATTCAGTG  
34801 TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG TGGGTGAAGA  
34851 GTATTCACAG TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG  
34901 TGGGTGAAGA GTATTCAGTG TGTGCAGGTG TGGGTGAAGA GTATTCACAG  
34951 TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG TGGGTGAAGA  
35001 GTATTCAGTG TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG  
35051 TGGGTGAAGA GTAGGCTGTC CAGGATTTCA ATCCTTGGCT TTTGCTCTGC  
35101 AGCAAGGGCT GGCTGAGGGC ACTGTGAGGC TTCTTCAGGC CCAGGAGTCA  
35151 GGCCCACTTT CCCTTTTCTC TTGAGGGAAT GACTCAGAGA AACTCCTGTC  
35201 CACCGGAGGT TCTGCAGGCT TTTGAGAGGC AGCCAGTGGA GGCTGATGGT  
35251 AGCAGTTGGT GAGAAAGAGG AAGTATGTAG TGGCCATTCC TCCGGCCACT  
35301 CCTGACAAAT ATTTCTGTCA CTAAACAGCA CCTCTCTGTG GCAGCCTTGG  
35351 GCTGTGTTCT GGAAAGGGAG GAGCTTTCTC CTCECTGTGG GAGGGCCTGT  
35401 CATCTGTGGC TTCTGCTTTG CCCTTGGCCA CAGACTAGAT TGCACAACAC  
35451 AGCCAATGAG AGTCCCTCTT CCCTCACAAG TGCTTGGAGT GCAGACCTTA  
35501 ACTTACAGGG TTGTAGAAGT GACCGTGTTT CACACTGCAG GGTCCAGGTC  
35551 ACAGCCGGCA AAGCACATGA AAATTGACCT AAGGTTAGAA TGTGATTATC  
35601 CTA CTGGGAA AGGTTTACTG GGACAGCATT TCACTTCTGA CTCCATAGGC  
35651 TGTGCTCTCC TGCCAGGGAG TGAGTTTTGT TTCCATGCTT GTCCAGTCTT  
35701 TACTGCTTTC CCAGAGGCCA TAAACCTGCC TTTTCCCAGA GGCCATAAAC  
35751 CTGCCCACCT CCTGCTATGT TCTAGTTCTG ATAGGAGTAC CATTGAGAGT  
35801 TCTTGGCAGG GGACCAACCC GCTTCTACCG TGGTTGGTTT CCCCTCCTTT  
35851 TCCCAGCTTG TTTGATGTGC AC GTTCTCCA AAATTCTTAT GCAGCTGGTT  
35901 GGCTCTGTAG TGCCAGAGA TTGGAGCTCC TGCAACGGGA ACCCCGCCGC  
35951 TTCCCTCCCT GGTTTTAGGG GCAGGGCTTG AAAATAAAGA ATCATAATCT  
36001 CCCTCCTCC TCCTCCTCCT CTCCTCCACT TCTCCCTGCC CCCACCCCA  
36051 CCCCCACCC CACCCTGCCA GGCAAAGTGG AGTGACCAGC TCAGAGCGGG  
36101 ACTCAGTCCA CCTCCCTGCT CTGCATGTCA GCAGTGATCT GGAGGAGATT  
36151 CCGGGGCGCA TGAGTATGTG AACTCTGGAG CACGTTACTG TCCCAGGCTG  
36201 GCACTCTGTG GCAGGTGTGT GCACTCATTG TGCTGTTACT GGAGACCAGT  
36251 CTCCTTAGGG GTGATGGTGA CCCAGCTAGA TGTCTGCCAG GTCTGTCCAA  
36301 GGCCACCCTG TTCTCTAATA GCTTGGGAAA TGGAAAGCAC TTCTAAATAC  
36351 CCCTGCTCTT CAGAAGAGCT GGCTGGGTGG TTTGGGGAGT TTCTTCTTTG  
36401 AATCTCTTAG AGTACAATAT CCCTTTTTTC CCGAAAGCCA GGTTCCTTAG  
36451 TTCCTAAGCT CCATTCTCTT GTTGCTAACT TACTACCTTC AGTTTTCTTA  
36501 GGTTGGGTGC ATCTTCCCTG GCCTCAACAA GACAGTGGCT GAAAGGTCAA  
36551 GAGAGTGGTA GCTGCTCCTT TGAGAGAAAG GGGATGTTGG AGTGGGAGCA  
36601 CAGGCTGCCA GCAGTTGTTT CACCTTCCCC CTTTGGCTGG CTAGGAAAGG  
36651 GGCACCACTT TAGTCTTCTG CCAACCTCCA CAGCCAGCTG TGGGAAAACC  
36701 CAAAAGGAAA CATCCTCTCG CTGCTAAGAC TTGAGAGCCT GAGGCAGAGA  
36751 CCAGCCAGTA GCAGCCCGAC CCTGCTGAAT GGGGAGGATT GTTTATTTTA

FIGURE 3A-16



36801 TTTTATTTTT TTCTGAGACG GAGTCTTGCT CTGTTGCTCA TGCTGGAGTG  
 36851 CAGTGGCGCG ATCTCGGCTC GCTGCAACCT CCACACCCCA GATTAAAGCG  
 36901 ATTCTTCTGC CTCAGCCTCC CGAGTAGCTG AGACTGCAGG CATGCGCCAC  
 36951 CACGCCCAGC TAATTTTTGT ATTTTAAATA AGAGACAGAG CTTCAACATG  
 37001 TTGGCCAGGC TGGTCTTGAA CTCCCGAACT CAGGTGATCC GCCTGCCTCG  
 37051 GCCTCCCAGG GGACTGGGAT TACAGGCATG AGCTACTGTG CCCAGCCTGA  
 37101 AGATTGGTTA TTTAGGGGCT GTGACAAATG GTTTTGCAGA GGAGCACTGG  
 37151 AAAGCCTGTA ACTTCACAGA GCCAGGGGTC AGCTTTTGTG CCATAGCCTT  
 37201 ATAGCTTCTG TGGCCTGTAG TGCCTGAGGC CAGGGGATCA GGTGCTGACC  
 37251 ACCTTTCCCT CTTCTTCCT GTGTCTTGCG GCCAGCGACT GTTATTGTCA  
 37301 GGTTGACCCT CTGGTTAGAG AGGATGACTT TGGCCTGGTG TCCAGACTCC  
 37351 CTGCTGCCTT ATCCCCTCTG CCCTGGAAT GCACCTAAAA ACAATTACTT  
 37401 TCCTCCTGAT TCCAACATAA GTGGTCACAG AAAGTTCTGT TTTGGCATT  
 37451 TGATTTCTGA TTGGGAGTTT AGGCATCTGA GAATTGAATG CTTGCTTTAT  
 37501 ACAAATATAC CCTTAAGACA TCTCCTCTTT TTTCAGCCCT ACATGCTTTG  
 37551 CTTGGGTATT AATTGAACCT GGGGCTTTTT AGGGACCTTA TGTGCTAC  
 37601 CTTCTAGTT TCCCCTCCAC TCCACCCCA AAAAACCCAA AGAACATTGG  
 37651 AAAAATTGAG CAGTGCCTCA AGGTCATTG ATCATAAGTG GTATTGGCA  
 37701 TAGTTAACTG GTTTGGTGTT TGGTGAGAGA TTTGTCTTT ATATTGAGC  
 37751 AAAAAATTC TTGGCGGGAG GCCTCTATGC TGTGTTGCCA ATGCTTGCCC  
 37801 TGTGCGCAGG GTTTGCCCCC TCCCCTCCCT TGACAGGTTG TTCTAATCCC  
 37851 CTTGTCTATA AACAAGTGCA GCAGAACTTG TCGGCCCAGC TCACATGACC  
 37901 TTGGTTATCT CTTTAACCAG CATCAGCGTT AGATACCACG GTCATTGAC  
 37951 ATGGTAGAGC TGTCAGGGTA GAGTGGAGAT ACCAGCAGGA ATCCTGGTCC  
 38001 ACGAAGAAAG GTAAATGGGA GTGTGTGTGA GGCCTTAGGA CTGGGTGGGA  
 38051 AAAGTCTGTT CCCATGGGGT AGGGCTTTCA GCTGTGAGAA GAGGATAATT  
 38101 TCATTCTTC TCCTTTTTTA AGAGACTGTC TCACTCTGTC GCCCAGGCTG  
 38151 GAGTGCAGTG GTCTAATCAA GGCTCACTGC AGCCTCAACT TCCTTAGCTC  
 38201 AAGCAATCCT CCTGCCTCAG CCTCCTGAGT AGCTGGGACC ACAGGTGCAT  
 38251 GCCACCATGC CCAGCTAATT TTTTTTTTTT TTTTTTTTG AGGTAGAGTC  
 38301 TCACTCTGTC ACCCAGGCTT AAGTGCAGTG GTGCGATCTC GGCTCACTAC  
 38351 AGCCTCAGCC TCCCAGGTTT AAGCGATTCT CCTGCCTCAG CCTCTTGAGT  
 38401 ACCTGGGATT ACAAGTGTGT GCCACCATGC CCAGCTAATT TTTATATTTT  
 38451 TAGTAGAGAT GGGGTTACAC CATGTTGTTT AGGCTGGTCT GAAACTCCTG  
 38501 ACCTCGTGAT CCGCCCACCT CAGCCTCCCA AAGTTGTTGG GATTACAGGC  
 38551 GTGAGCCACC ACGCCCAGCT AATTTTTCTT TGTTGAGATG GGAATCTCA  
 38601 TTATGTGGCC TAGGCTGGTC TCGAACTCCT TGCCTCAAAT GATCCGCCTA  
 38651 CCTCAGCCTC CCAAAGTGCT GGGATTACAG GTGTGAGACA CTGTGGCCAA  
 38701 CTTTCATTCC TTCTTTATCA CCCTAAAATT TCTAGTTCTG GCGTCTTGTT  
 38751 TATCTTTCTC AAATCCTGTC TGCAGGGGCC CAGGACATGC AGCTGTTTCA  
 38801 GGAAACCGCC CTTGAGATGG GGCAGATGTA TGCTAGTTCA TGGGCTATAA  
 38851 AACTCAACAC CAAAAATCCC ATCGTCCTAA ACAGTGACCT GTTATGTTGT  
 38901 GTGAAGGACA GTGGCGATGG GGGCCTGGCC GCCAGAGAGG CTGCTGGATT  
 38951 CTATGGCAGA CACACTCAGG AGCTGGAAGT GTGGCTAAGC TTTCAGCAGC  
 39001 ACCATCACTT CCCTCCCCAT ACACATGCAC ACAGGTTTCC TTTGTCTCAC  
 39051 AGCTGAAGAG GCAGCGCCCA GCTTCAGTAA GCACTGTGTA TGAGAATGGA

FIGURE 3A-17

39101 CTTACTCTGG CCACACTGTG CACACGCATG TGTGTGTAAG AACTGATCA  
39151 CATTTCCCAT AAAGACTGTT GATTTGCAGA GTTCCAGGC CCATACATCT  
39201 AGGGCGGGAT GTGTGTGTTT TCATCAGGGG AGAGTAGAGT GGCCTTTTGT  
39251 GGAAGGGATA AAATGGTTGA GCTGCTGGAG ACTTTTCTAG CTCCATTTAT  
39301 ACAGCAGCCT TTCTGCCTGG GTGCAGACTT GAACCCAAGT CCAAGTTCAA  
39351 GCCATGTGTG TAGATGACCA GAACTTAGCC TTCAAACCTA GCCTTCAACT  
39401 TCAGGACTCT CCTGGAGAAA ACATCCATCT CCTTTTGGAG ATACAGAGAA  
39451 TTCGTGATGA GCTTTGAGTA CAGAAGTTCA AGTTATATTT TCTGGCAACC  
39501 TACAGAATAA GTTGGGAAAG GATATGTAAT TATAGAAATA ACCAGCATGT  
39551 CGCCAGGCAT TGTGTCCGT GCTTAGATG GTGTGGATAT TTTGTAATTT  
39601 CTGATTCTTT ACCTACTGTT TTCAAGACTT GGTAGGGACC CCGTTATGGC  
39651 TGTGGGGTTC TTTGTCCTTG GTAGTTAGCA TGAACATATG AGAGCAACAG  
39701 AATGGGTAGC CGTGGCCTCT GGCCACCCAG CTAAATTCTA CTGATGAGAG  
39751 GTATCCTGGG TGGGTTTCTT CTTTGGGTCT TCGTTTATGC CGCCATTCTT  
39801 ATTGCCAGTT AGAGCTGCCT TTTAGGATTT GTTGGGTAGG AGCTGTATTC  
39851 CTCTTGGAGC CATCTTTTCT TCCCTGCCAT CTCTGAGTGA ATTCAGAGGT  
39901 GGAGAGCTAC AGACTTGGCT GCTTGCCTCC TTCAAAACAC CCAGCATTEC  
39951 CTTGTCCACA GTCTGTGTAG CAGCACATCT AACAATGCCC AAAAGCGGCC  
40001 CCCTTCCTCC CAGCCACTTG TTAATGGGTG GTTCTGGTTC CTGAGGGCTT  
40051 CGACCACTGC ACGAGCTAAT CTCCTGAAG AGTGCCATTC CCAGGTTTCT  
40101 ACCACAGAAG TTAGAAAGCT CAAAGCCCAG GTCTTCTGCA CCGAAGAGTG  
40151 CCATTCACAG GTTCATACCA CAGAGGTTAG AAAGCTCAAA GCCCAGGTCT  
40201 TCTGCTGCCT TGGGCCATTC CCTTCTCTTA GAAACCAGTT CAATCAGACT  
40251 CTTTTTTTTT TTTTTTTTTT TTTTTTTTGA GACGGAGTCT TGCTCTGTCA  
40301 ACGAGGCTGG AGTGCACTGG CATGATTTCT GCTCACTGCA GCCTCGACCT  
40351 CCCCAGGCAC AGGTGATCCT CCCACCTGGG CCTCCTGAGT ACCTGGGACT  
40401 ACAGGTGCCC ACCACCACGC CTGGCTGATT TTTGTATTTT TAGTAGAGAT  
40451 GGGGTTTCAT CATGTTGGCC AGTCTGGTCT CGAACGCCTG ACTTCAAGTG  
40501 ATCCGCCCCG CTCAGCCTCC CAGAGTGCTG GGATTACAGG CGTGAGCCAC  
40551 TGCACCCAGC CCAGACTCTT TTCATAGGAT GCTGAAAGGA TGAATTAAGT  
40601 ATAAAAAGTG CCTTTTGGCC AGATGCAGTG GTCATGCCT ATCACTTGAG  
40651 AGGAGCTTGG GCAACATGGT GAAACCCCAT CTCTACAAAA AATACAAAAA  
40701 TTAGTTGGGC ATGGTGGTGG GCACCTGTAG TCCCAGCTAC TCAGAAGGCT  
40751 GAGGTGGGAG GATCACCTGA GCCTGGGGAG GTCGAGGCTG TAGTGAGCCA  
40801 AGATCGCGCC ACTGCACTCC AGCATGGTGA CAGAGACCTT GTCTCAAAAA  
40851 AAAAGTGCTT TTTAATAAGG TACACGTAAT GGAAAATGGC TGTCATCTGG  
40901 TTTGCCATAC TCTGCTCCTA GGTAGAAAGT ACAAACAGCA AGGGCCCCTT  
40951 GGAGCAAAAT TGTCATTGCC GCCAGTGAAT AAACAGCAGT GGTTGGCTTT  
41001 GAGGGGCACC TTCAGCCTAA AGCCATAAGC TGACATATAC TCAGTCTCAC  
41051 TGAGAAGCTC GGGCTTTCCA CTGTTACCT AACTGCTGAC AAATGAATCC  
41101 TCCATTGATC TGGCAAGCTG GCCAGGATAC CTGCCCAGGC CATGGCCACT  
41151 TAGTAACAGG ATCCGGTTCT CAGTGCAGGG TTGAGACTGC AGCAGCAGTG  
41201 GCAAGCCAG TAAGGCAGGT ATGAAGCACA GCCCCCGCAT CGGTTGCCTA  
41251 GTAGGGAAGA CAGTTGTAAG GAGCATTTGC CCCTGTTATG TCAGGGTACT  
41301 GTTGCAAGTT GTCTTTTCTC CTCTAGCTGG AAGTTGTTCT ACCCAGTCTT  
41351 CCTTAATTAG CTCTCTTTT GTGTAAGGCA GCACCCATTT AAAATTCTTT

FIGURE 3A-18

41401 TCCTCCAGCC TCATTCCTCA TCTCCATTG GGTATATATC TCCTCAGAAC  
41451 CTCTCTCCTA CCCAGCCTTA AGCTCTACCC CAAATGCTTT GAAGCTCTCT  
41501 TGTTCAAGTC TTTTTTTTTT TTTTTTTTTT TTTTGTAGAC AGAGTCTCTC  
41551 TCGCTCTGTC GCCTAGGCTG GAGTCAGTGG CACGATCTCG GCTCACTGCA  
41601 AGCTCCGCCT CCTGGGTTCA CGCCATTCTC CTGCCTCAGC CTCCCCGAGTA  
41651 GCTGAGACTA CAGGTGCCCA CCACCACGCC CGGCTAATTT TTTGTTTTTT  
41701 TAGTAGAGAC AGGATTTTAC CGTGTTAGCC AGGATGGTCT CGATCTCCTG  
41751 ACCTCGTGAT CCACCTGCCT CGGTCTCCA AAGTGCTGGG ATTACAGGAG  
41801 TGAGCCACCG CACCTGGCTC AAGTCTTCTT GATTCAAGCC CTCACCCAGA  
41851 GCTTGAAGAC TAGGGAGCCC CCGTGTCTGC TGCCCATGGT GCTTGGAGAG  
41901 CAAAGATCTG TTCCCGGGTC CTGAGTTGGA ACTCTGAATT CATTTCTCTG  
41951 TCTGGGCTAT GGTTTAAGTC TTAAGTACAA TTCACGTACC CTTGAAATA  
42001 CTATGCTGGG ACCTCATGGG CTGGCCTGAG AACACAGCTA CCATTTGTAA  
42051 CATGTTTCTA TGGAAAAAGA GTTCCTTCTT AGAACAGAAC TTTTGGAAC  
42101 TTGGGGATTT CTTGACTAAT ATGCTGCAAC AGATTTGCAT TTGCCTGTGG  
42151 AAGTGTCTCT TTATTTTGTA TTCAGCTGGG CACGGTGACT CACGCCTGTA  
42201 ATCCCAGCAC TTTGGGAGGC CGAGGCAGGC AGATCACTTG AGGACAGGAG  
42251 TTTGAGACCA GCCTGGCCAA CATGGTAAAA CCCATCTCT ACTAAAAATA  
42301 CAAAAAATA ATCTGGGCCT GGTGGTGAGC GCCTGTA CT CAGCTACTC  
42351 TGGAGGCTGA GGCAGGAGAA TCACTTGAAC CCAGGAGGTA GAGGTTGCAG  
42401 TGAGCTGAGA TGACACCACT GCACTCCAGC CTGGGCGATA GAGTGAGACT  
42451 CTGTCTCAA AAAAAAACAT TTAATAATC ACATTTTG TG GTCATGGCAC  
42501 TATCTATCAC ACAAGTAAGT TGTCTCTCTA TATGCCAAAT GACAGAAAAG  
42551 AAGCACCTC CTCTCCAC CCAGAAAGGT TGCTAGAGAG CTACCCTTGT  
42601 CTTCTGTGAT TGCCTTGAGG GGCAGGTTTG TCTGGGTTCT CCATGTCAGC  
42651 TGATTTGATC CATAGTCCAG TAGCACCTGA AACAGGATGC CCTCATTCCA  
42701 CAACTTAGGT GCCCTCTCCT GCTTGGTTTT TTAATGATCT GCTACAGGAG  
42751 AAAGATAGCA CCTCTCCCTT CAGCAGGAGC AGCCCAGTAA GGGCTTGCTT  
42801 CTAGAAAGAT TGGCCAGTTG GATTTTTAGT GGTCACCTAA GTGGAGTAGC  
42851 CACTTTGCAG CCTGGCCCAA CAGGGAGACA GTTCTGAGGT GAGGGTGGCA  
42901 GTGACAGCCT TGGGGTGTT TCTGATGTGC TCTGACCTCT GGCCATGGTG  
42951 ACTTCTGGAG CAACAACTT TGTCCCAGTA TTTTTTCTG ACATTTCTCT  
43001 CTCCTTATTC AACTCCCTCT TTGAACTGG AGGAGTAGGG AGGCAGTATT  
43051 TGTTCACTTC CAGAGAAAGA TGCAGCAGGA AGAGGCATAT GTCTTGTCT  
43101 GCACTTTCCA GCAGCAATGC TGGGACTAGG GGGCTAGAA GGCCTGTTTC  
43151 CCAGCTCCAG GCTGGATCTT ATCCTCAGCA TACAAGCAAG TTTTAAGGAA  
43201 ACAACATTGG AAAGGGCAGA AACAAAGGGT TAAATCTGTA CCCAGGTAGA  
43251 AAGACTGTTG CATAAATGCT GAGTTTTTTT TTTGTTTTTT TTTTAAGAT  
43301 CTCATGCTTC TTTTTTACTT TGTGTTGGCA AAAACCCAG GAGAAGATGG  
43351 GAGATTCTGG GAGGAGATGA TTATGCTGGG TGAGTCAACT GAGCTCCCCA  
43401 GCTGCCGTTT TTAGTCTTT TGCTTTCTG TAACAGGAGG CAGTTTGGGG  
43451 AGGGGTGGG GGCAGGGTGG GAATGCTGAT TTTTGCAGCA GGACAGGAGG  
43501 CAGGTGTGTA TGGGTGAAAT TATTTTGACA CCCTAGAGTT AACCGGGCCT  
43551 TAGAGTCAGT ACATTGGTTC AAGTAACAAA TATCAAAGCA GAACTCTTAG  
43601 TGTGGCAAAC AATAAATAAT TGTCTCCTAG ATTCTTATAC AAGTCACTGT  
43651 CCGTCCCCAA TTGGTAGCTC TTAGAATGGC TCGAGTTGCA TTCATTGTCA

FIGURE 3A-19

43701 CAGCAAGACA CAATGGTTTT GATAGCAAAG CAGTAGAGAA ACTAAATGTA  
43751 GAGAGGCAGA GAGAACTGTA TTAAGTCTGA GGACCTGGTG GTTGTCTATGG  
43801 GCAGCAGGAA GTGTGAAGGA GAGGGTTTTT CCTCCGATGA AAGGAAGGCT  
43851 AGGGCTTGAT TCAGGGGAGC AAGTGGGATG GGCCCTGCTG GTCCCTGGCT  
43901 GTGCCTATAT TCTGAGTCTG TCTCCAGCTC ACCTTGGTGA TCACTCACTT  
43951 TTCATCCATC ACTGGGATAG GGGATCTCGT GGCTCATTAC CCTCATGGGT  
44001 ATTTTTTGCA GAGTACACTG AAGTGGGCTA TCAGTTATCA GTTGGTCCCA  
44051 GAGACCGTCA TGAAGACATC GCAAAATGTT TTCTTATGTA TTCATTTGTG  
44101 CACATTTATT AATTCAGTAC TTTACTGAAT ACTGTGCTGG GCATTGTTCT  
44151 GGGCCATGAA TAAGACAGAC CTGGCCTGGT GCAGTGGCTC ACGCCTGTAA  
44201 TCCCAGCACT TTGGGAGGCC AAGGCAGGCA GATCACCTGA GGTGAGGAGT  
44251 TCGAGACCAG CCTGGCCAAC ATGGTGAAAT CCCGTCTACT AAAAAAAAAA  
44301 AACAAATTAG CCAGGCATGG TGGTGGGCAC CTGTAATCCC AGCTACTTGG  
44351 GAGGCTGAGG CAGGAGAATC GCTTGAAGTC GGGAGGCAGA GGTTGCAGTC  
44401 AGCCGAGATC ACGCCACTGC ACTCCAGCCT GGATGGCCAG AGAGAACTC  
44451 TGTCTCAAAA AAAAATACCA AGGTCCCTCC TTTTGTAGTG TAGTCTAGCA  
44501 GGAAGGACAG ATAGTAACCA ACCAACTTCA AGGGCAACGA ATGCCTCGAA  
44551 AGAGGGGAAA TGGGGCTGGT AGCAAGAAAT TGTGATCTTC CTTCTCTAC  
44601 CCTTATCTCT TGGGGTCGAG AGTGGGGTCG AGAGTGGGCA ACTTTAAAGA  
44651 TCAAAAAGTT GTGCCTCTCT TGTTCCCTAA GTATTGTAAC ATGGGTCAGC  
44701 TAGGTGTGGG CACTGTTGGG CACTGAGGGT ATATGAAGGT GAGGGAGATA  
44751 CTGGCTCTCA TCTGTCAGAG CATGAGGGGG TTAAGGTATG GGGACACAAA  
44801 CAAGAAATCA ATGGGGCTGG GTGTGGTGGC TCACGCCTGT AATCCCAGCA  
44851 CTTTGGGAGG CTGAGGCAGG AAGATTGCTT GAGCCTAGGA GTTTGAGGCC  
44901 AGCCTGGGCA AGATGGCAAG ATGCCATCTC TACAAAAAAA ATGAAATAAA  
44951 TAAAAAACTA GCCAGGCATA GTGGCACACA CCTGTAGTCC CAACTATTCTG  
45001 AGAGGCTGAA GCAGGAGAAT CCCTTGAACC CAGGAGTTTG AGGATGCAGT  
45051 GAGCTGTGAT TGTGCCATTG CAGTCCAGCC TGGGCAAGAG AGCAAGACTT  
45101 CATCTCACAA AAGAAGAAGA AATGAAGAGT ACAGATAGAG CGCTGAGAGT  
45151 CTAGAGAAGT GAGTCTAGAG AAGTGAGTGA CCACTCCCCG CTAAGACGGT  
45201 GTCTGGATTT GAGATAAACA ACGGATAAGA GGACTTACCT GGATCACAGG  
45251 AAGGCGCATA GGATAGATGA CCACTTTCCT TTTAGTATGT GTAGATCTGG  
45301 GTAGCTCTTT GTACCACAAT TCTGACCCAT TCTTTTTTCT TATTATTTTT  
45351 ATTTATTTAT TCAAAATAAT AATTTTTTTT TTGAGACAGT CTTGCTCTGA  
45401 GCCACCATGC CCAGCCTGAA ATAATAAAAG TTTTAATCTT TAAAAAATA  
45451 TGGGCCAGGC TTAGTGGCTC ACACCTGTAA TCCCAGCACT TTGGGAGGCC  
45501 GAGCTGGGCG GATCACCTGA GATCAGGAGT TCGAGACTAG CCTGACCAAC  
45551 GTGGAGAAAC CCTGTCTCTA CTA AAAAATAC AAAATTAGCC GGGCATGGTG  
45601 GCGCATACCT GTAATCCCAG TTA CTGTTGGG GGCTGAGGCA GGAGAATCAC  
45651 TTGAAACCCG GGAGGCGGAG GTTGCACTGA GCCGAGATCA CGCCATTGCA  
45701 TTCCAGCCTG GGCAACAGGA GCGAAACTCT GTCTCAAAAA AAAAAGGAAT  
45751 GCTTCACAAA TTTGTGTGTC ATCCTTGAC AGGGGCCATG CTAATCTTCT  
45801 CTTTATTGTT CCATTTTTTT GTATATGTGC ATGTACAGAG TAGTGGAGCT  
45851 GGGTTATCAC TACAGTCTAA CTCCAGAATG ACACCCTTCA CTA CTATAACC  
45901 ATATATGGTG CCCAGTATA CAGCAGTGA GCTAGGAAGA AAAGCCCAGT  
45951 GTCTAGAGAG CCCAGAAAAT ATGCCAAGAA CATATATACT AGGCAAAGAA

FIGURE 3A-20

46001 AACGAGGTTA GGAGGAAGCC CAGCCACCTC AGCTGCACTG GTTAGGATCT  
46051 GCTGCCTCCC CACAGTCCTC TGTAAGTGA GCCAGACCTC TATGCTGCAG  
46101 GCTTCCTTCT GCCTACCCCC ACCACCCCCA TCCCCCAGAG CCCTGGGCTA  
46151 CTGGCAGGCT GGCTCTCCTG TGATATGGAG GAACTTGTTG GTCTCCATGG  
46201 TTACGGTAAC CCACTGGTAT GGGAGGAACC GCATAAAGTG CGAGGCTGGC  
46251 AGTGTGAGCT TCCCTCAGCC CTTGGCACCA TGTGGTACTG GTATGTCGGC  
46301 TGTTTCATGG ACCTTTTCTG GGAGGAGGGA GTTAAGGAAC TGATGAAGAA  
46351 GGGGAAGAACC CTGGCAGGAC CACTGTCGTC ATCCTCTGGG CCACACAGAG  
46401 GGCGAAGGCA TGGGCACCAT GTCATTGAGC TACTCCTCCT GCAGGATGGT  
46451 TTTATGTTAG GAAAGAGGGT CCTCTTTGCC TGATTGCCCA GCCATGGCAG  
46501 AATTTGACTT TTCCTTGTTA TAGAGGGAAT ACCAGGATGA CAGGAATCAA  
46551 CTTAGCTATA CTGGTACTTA CAGTCAAATT TCTAGGTATT GTAGCTCTTC  
46601 CCAGAGCCCA GAGAACCCTT GGAGAGGGGA AACAATGGTT CCTACCCAAA  
46651 AATGAAGCTA GATAATAATA GAATACATCA TCAAGACATT ACTGAACACC  
46701 ACGTTCTATG GTAAACACTG ACATGGATT TCTTTTTTTT TTTCTTTTGA  
46751 GACAGGGTCT TACTCTGTCA CCCAGGCTGG AGTGCAGCAG TGTGATCAGC  
46801 GCTCACTGCA GCCTCAGCCT ACCTCCCTGG GCTCAGGTGA TCCTTCACC  
46851 TCAGCCTCCC AAGTAGCTGG GATTGCAGGC AGTTGTCACC ACACCCCGGC  
46901 TAATTTTTGT GTTTTTTTGT AGAGCCTGTG TTTTGCCATG TTGCCCAGGC  
46951 TGGCCTCGAG TTCCTAGGCT CAAGGGATCT GCCTGTCTTG GCCTCCCAAA  
47001 GTGCTGGAAT CAGAGGTGTA AGCCACCACG CCCGGCCAGA TTTTCTCATT  
47051 TAATCTTCAC TCTAATTCTG TGAAATGGGT ACAGCTAGTA TCTTTATGTC  
47101 CCAAATGAGG AAACAGATTT GGAGAAGTTA TGCACTTTG CTCATGTTCA  
47151 GTCAGCTGGT AAGCAACAGA GGTGGGCAGA GCGACTATAG TAAGTTTTCT  
47201 GTATAGTTTA CCTCTTCTAA GTTCTGGA GGCAGGAGCC AGATCGCACT  
47251 GAGCTTTGCA ACTGGAGCCA GGGCTCCAGA GTACTGCTCA ACAAAGGTTT  
47301 GCTAGGGCAA CAGTAGCTGG GGATTTAGCG ACCAGACCCC AGCAAGCAGA  
47351 TTCTCAGGGA TGAAAGTAGT CCTGGAAGCC TCTAAAGCCC TGGTTGCTCA  
47401 GTAGAATCTA GTTTCAAGAG GAGCCCAGCA TTTCAAGTGG CTCTGAAGAC  
47451 AGAGGAGATT TGGAGAGTGC TCTTTGCATT GTGGCTTCCA GGCTGAAGG  
47501 AGAGTGAGCT GGAGGTTGCT CTCTGTTCTC ACCTCTTATG CCATGTCAGG  
47551 TTTTTCCTAG GCAGGCTTGA GTCCTGGGGG AGCCCCGCCT CATGGCCCAG  
47601 GCTGCAGTGC TGATCTCCCT GCCTTGTTGG GAGGATTGCA GCTCAGAGAG  
47651 CTAAAGGGCA GTAAACCACC TTGGTTTTGG CTTTGTGCTT AAGTTGCAGG  
47701 CTCTTCTGGT TATCCTTTGT GAAGGAGGCT CTTACCCTGG CTGGAAAGAG  
47751 GGAGCAGCCC CTGCCTCCCA TCTACAATGG GACAGTAAAG GAATATGGCT  
47801 GTTTCTCAAG TGGAAACAGT ACAGTTAATT TTGGGGGTGG GAGCATCCAG  
47851 GCTTTCCACT GGTGAGTGCC TGCCAGTTTT ACAAGCTCTC CTACACTGAA  
47901 TGCTCCTCTG GTTTATTGAC TCTTGCGAGT TGATAGCGAT AGTTGCTCAT  
47951 GGCAGTTGAT AGCGATAGTT GCTCAGAATC AAAGGATGAA AAGACAGTTT  
48001 CTGGATACAG TGAGGGAGGA AGGGTTAAAA AACAAAGGAC TCCAACCTCC  
48051 AGTTACGAGA TGTCCCATAT GGCCATGCGC AGTGGCTCAC TCCTGTGATC  
48101 CCAGCACTTT AGGAGGCCGA GGTGAGAGGA TTGCTTGAGC CCAGGGAGTT  
48151 CGAGACCAGC CTGGGCAACA TGGAGAAATC CTGTCTGTAC AAAAAATACA  
48201 AAAATTAGCC GGGCTTGTTG GCCCATGCCT GTAGCCCCAG GTATTCAAGA  
48251 GGAAGATCAC TTGAGCCCAG GAGGCGAAGA TTGCAGTGAG CCAAGATCGT

FIGURE 3A-21

48301 ACCACTGCAC TCCAGCCCCG GCAACAGAGC AAGACCCTGT TAAAAATAA  
48351 ATAAATAAAT AGGGACTTGC CACAGGCACA TGACCTTTCT TAAGAGACAA  
48401 AGTCTTGTGC TGGGAATGGT AGCTCATGTC TATAATCCCA GCACTTTGGG  
48451 AGGCCAAGGT GGGCAGTTCA CTTGAATTGT TGAGTTCAGT ACCAGCCTGG  
48501 ACAAGCTTGC AAAACCCCTAT CTCTACAAAA AATACAAAAA TTAGCCGGGC  
48551 GTATTGCTGT GGGCCTATAG TTGCAGCTAT TCGGGAGGCT GAGGTGGGAG  
48601 GATGGATTGA GCCCAGGAGG CAGAGGTTGT AGTGAGCCAA GATCGTGCTG  
48651 CTGCACTCTA GCCTGGGTGA TAGAGTCATA CCTTGTCTTG AAAAAAAAAG  
48701 AGAGGCTGGG CGTAGTGGCC CATGTCTGTA ATCCCAGCAC TTTGGGAGGC  
48751 TGGGGCGGGT GGATTACTTG AGGCCAGGTG TTCAAGACTA GCCTGGCCAA  
48801 GGTGGTGAAA CCCCATCTTA CTA AAAAATAC AAAAATGATC TGGACGTGGT  
48851 GGCACGCACC TGTAATCCCA GCTATTTGGG AGGCTCAGGC AGGAGAATCA  
48901 CTGGAACACA GGAAGCGGAG GTTGCAGTGA GCCGAGATCG CACCACTGCA  
48951 CTCCAGCCTG GGTGACAGAG CAAGACTCCA TCTCAAAAAA AAAAAGAGGC  
49001 CGGGTGCACT GGCTCAGACC TGTAATCCCA GCACTTTGGG AGGCCAAGGT  
49051 GAGCAGATCA CAAGGCCAGG AGATCGAGAC CATCCTGGCC AACATGGTGA  
49101 AACCTCGTCT CTAATAAAAA TATAAAAAAA TTAGCTGAGT GTGGTGGCGG  
49151 GCGCCTGTAA TECCAGCTAC TCGGGAGGCT GAGGCAGGAG AGTTACTTGA  
49201 ACCCGGGAAG CAGAGGTTGC GGTGAGCCGA GATTGCGCCA CTGCACTCCA  
49251 ACCTGGGCAA CAGAGTGAGA CTCTATCTCA AAAAAAAAAA AAAAGAGACG  
49301 AGAGTCTAAT TCTGTCACCC AAGCTGGAGT GCAGTGGCAC GATCATAGCT  
49351 CACTGTTACC TCCACCTCCT GGA CTGAAAC GATTATCCTG CCTTAGCCTC  
49401 CCGAGTAGCT GAGACTACAG ACCCATGGCA CCATGCCTGG CTAATTTTTG  
49451 AATTTGGAGA GAGAGGGTCT CACTCTGTTG CCCAGGCTTG TCTCGAATTC  
49501 CCAGGCGCAA GTCGTCTTCC CACCTTGGCC TCCCAAAGTG CTGGGATTAA  
49551 GGCATGAGCA ACAGTGCTCA GCCCCGTGTG GCTTTTTTTT TTTGAGACAG  
49601 AGTCTCACTC TGTTGCCAG GCTGGAGTGC AGTGGTGCAA TCTCTGCTCA  
49651 CTGCAACCTC CACCTCCCAG GCTCAAGCAG TTCTCATGCC TCAGCCTCCG  
49701 AGTAGCTGGG ATTACAGGTG TACGCCACCA CGCTCAGCAA ATTTTTGTAT  
49751 TTTTAGTGGA GATGGGGTTT CGCCATGTTG CTTAGGCTGG TCTCGAACTC  
49801 CTGACCTCAA GTGATCCACC AGCCTCGGCC TCTCAAAGTG CTGGGATTAC  
49851 ATGGTGGGGG CCACCATGCT TGGCCCCCAT GTGGCTTTTA ATCTAAATCC  
49901 TACCCTATCT CTTCCCAGCT TTTCTGTTT TAGTCAGTGC TTTGTATTC  
49951 CTCAGTTTAC AAAATCCCTT ACTGTCTCCC ACAAATAGGA TTGAGGAAAC  
50001 AGTCCTTCTG TCACATTGCA AAGCCCTAGA AAAATGAAGG GACTAGAAAA  
50051 ATGAAGCTGT TTGATCCTGC TCTGGTTCTC AGTCTACCAG TGAGTGAAGG  
50101 GCCGGAGGGC CCGGGCAAGC TTGAGCCCAG GATCCAGTGG GCCCACTGAA  
50151 GTCAGGGCCC ACTTTTGGGG GGCTGGGAAA AGGAAGGGTT GCTGTGGGAC  
50201 CACTGGGATA GGCCTTTAAA CAGCACTTCA CCATTGGCCT GAATCAAACA  
50251 TTGTCAATCC CAGTGTCCCG AGCACCTTCC CTGAGTCTTC ATACCTTCTG  
50301 CCTCCTAGCT TATGGAGGAG GAGCCAGGGG CTTATCTTTT GGGGGAAATG  
50351 AGAGCACGAT TAGGCATCAA GAAGGGTTGA TGAGAACTG GTAAGGGGGA  
50401 CTGTCAAGAA CAGCAGAGTG CTGAAATGGT GACAAAAGCT CTGGGCTCCG  
50451 GCCCCAGCTC TGTA CTGAGA AGCTGTGAGA TTTTGGGCAA GTCTCATAAC  
50501 CTCTGAATGC CAATTTCTCA ATGGA AAAACA GGGAGACTAC CTACCCTATA  
50551 GGTCTGTGTT TGGAGAAAAC AAAGTGTAAG CGCTGGACAT ACAGTAGCAT

FIGURE 3A-22

50601 CAGAAATGCT GAATCCGTTG GCCAGGGCTC ATGTGTAAGG CAAACATTTTC  
 50651 TTGGCCACTC CTGAGTAGCA TGGTCTTGCA GGAATATATG CTTAAGTGCT  
 50701 GTGAGAGCAC AGAGGAAGCT TTGCCCTTCC CTAGAGGGTT AATGGCTACC  
 50751 AACGTGAGAA GGTACGAGG TTCCTTAATG AGAGGGAGCC TAGCCTAGAA  
 50801 TAGGGGATGA ATGAGAAATT GTTCTGAGAA CCAGAGGCAA GGCTGCAACC  
 50851 AGCACATAGA CAGGGGTCGT TGGTCTAGAA GGGGAGTCTT CTCCAGATGA  
 50901 GAGACAGCCA GCTTGCCCTG TGCTCACCAT GTGCCCAGAT AGTGGGGGCT  
 50951 TAGCAGGAGG AAGGTGTGAG GAATCCCAGG CCTTTGGAAT TCCTTGAGAA  
 51001 AGCAGTGTTG TTTTGAAGGT AAGGCAGGGG ATTGGTGACT GGAAACTTGG  
 51051 AGGTGAGTGA GAACCTAGGG ATGAACGTTT AGAAGCAGGG CTGGAAGGAA  
 51101 CTTAAAAGGG ACATTTGGAT TGTTCCTAGC TTTTGGGCAA AATCTAGGAT  
 51151 TAAATATGAT TTTTTCATTG ATAGAATGCT CTATCAGTGA TAAAGGCTCT  
 51201 TAATCTAGAA AACATACACC TCATAGGGGG CTTTACAGAG TCCCCAAACT  
 51251 CCCTGAAATT ATGCTCAAAA TATTTTGTGT CTAAGTGGAA TGTGCATGTT  
 51301 TCCAAGGTTA AGCACTGCTT TTTTAGGAAG TAGGAGGTCC GTCCGCCACT  
 51351 GTCAGCTTGC TGGTTTCTGC TTACCCTCCT CCCCCTTCG TTCTTGAGGG  
 51401 GGTGGTTTGC TGGTCTTTGG CAGGGCCGCC ACTCTGGGTC AGCACATCTG  
 51451 AGTCACACAT GTTCCTCCCC AGCCCTATTG GAGGCTTTGT TAAAGTCATC  
 51501 TGCCCCCTACC CAGGTCCAC CTGCCACAGG TGAGCTAGGG TTTTATGACA  
 51551 GCCGTGGCTG CAGTGAGTCT CCTCGACCTC TCGCCAGCTG TTACCCAGCA  
 51601 AAGCACCTTG GGGAGGGTGG GGCTGCCAC TTCCGGGGAG GGAGGGAGGG  
 51651 GGAGGGGAGA AGGAAGTTGA TCTAAACCCG CCTCTTTCTC TGTCTCCCTT  
 51701 CCTGCCCTAT TCCCCTCCTG CCCCTTCCCT CCCACCTTGC TTCTGGTGTG  
 51751 CTGTCCTGGA ATTGCACGCG CTTCTGACC ACCAGGCTCT GGCCCTTGAG  
 51801 AAGCCAGCGG GGCTTTGTCC CTGTTGCTCT CCTTGCCAAA CCCAGTCTCT  
 51851 CTGCTAGTGG TGGTTTCGGT TGCACACCG TCCAGGTTCC CAGGCAGGAA  
 51901 CCGCTCGGCC TGGCTGCTTA GCTACTTTTC ACTGAGGAGG TGGTGAAGG  
 51951 TGTCGCCTGC TCTGGCTGAG TAAGGGTGGC TGGCTGAGCC GGCAGCCCCC  
 52001 GCCCTAGGCC TGGCTCTTCC CGGCCTCTGT ACTTTGCCCT CGCTGCCTGA  
 52051 CAGGTTCTGC TGTGGGCTCT GCTGAATGGA AGTCGCTGGT AGTCCTTTTC  
 52101 CCTTCTCCA GTCGGGTATG TTGTCCCCCT TTTTACTCTA GGATTGCCTC  
 52151 CTCCTCTTTC TTTCTCTCA TCTCAAACAT AGGATCTTTA GAGAGTTGCT  
 52201 AAGGGGCGCC CTGCCTGAGT CCAGCATAGT AATATTCATG GGAAGGGTGT  
 52251 CCAGATGTGG AAGAGGCATT GACTAGGAAA GGAAGAGGGG GCACATACCA  
 52301 GAAGGGTCTC CCCTGAGAAC AAGCAGCTTG ACAAGTGGGC GAGGAGGGGC  
 52351 TGGTGGGAGG CAGAGGCCTG AGGCCTCAGA GAGGATGCTC CCGTGCTACA  
 52401 GTGAGGGGGA GCCTAGGATC TGGGGCCATT GCCCAGGACT GGTGCCCAAG  
 52451 GGACACTTTT CTCCCCAAC TCTATAGTGC CTGGCTTACT CTGCTTCTGG  
 52501 CCAGGGAATA TCACCCCTCC TGGTTTGGCT CTTCTCAGC CCTCGGGAAG  
 52551 CCAAAGGACA CTTGAAGCCA GCCCTGAATG CAGAGCCCCA AAGCATGAGC  
 52601 TTCTCCATGG GACAACTGTT GGTAGGAGCC TCCAGCATTG GGGCAGGGGC  
 52651 CCTGCCTACC TGAGTCAGCG CCAGGCCTCT CGGGGTGGAG GCTGTCTTCC  
 52701 GGGCAAGCCT GACAACACAC CTAGGCCGAG TCTGAGATCC CAGGCGGAAG  
 52751 GGGCCTGACA GGCCAGTGG ATGCAAAACT ATCTTTTTAT TTTCTCCTCC  
 52801 ATGTCCTGCC TTCTCTCTTC CTCTCAGTAG CAGACCCCAA AGCTGTTTCA  
 52851 GCCCTACTTC TGAATCAGGC CTGCTTAGTA ACTACTTGGT TTGCCTTTTG

FIGURE 3A-23



52901 GTTCCAAATA ACTGCCTTGC AGGGTGACCC CTTATTCTTT CTAAAGGCTA  
52951 CTTGAGAGCC ATAGGGTCTA CTCTTGACAG ACCTCCTCCA TCCTTTAGGG  
53001 CCTGTCTAGA GTATGATATA GGCCAGAGCT TTGGGAGTGC CTGGTGTGCC  
53051 ACGTCTTACT ATAAGCAGGG AGGATGGTGG TAGAGGGGAG AGCGTGGCTT  
53101 TTGCCAGGTC CTATTGAGTT GGCCAGCAG GGCAGCTAAT CCTCAGCCTG  
53151 CCATCCTGTT GGTGAGACCC AGGGCCAAGC TGAATGGTGC AGCCAGAACC  
53201 AAAAAAGAGA AACTCTCTCT CCATATTAGC CACTGCATAC TCTTACCTCT  
53251 TTATCCTTCA GGAAGAAGC TAGGTGAGGA AGTTGCCTCA CTTGGGGCCT  
53301 TGGCCCAAGA AGCATTTCTG TTGGAGACTC TCTCCTCTCT TTTCCCTTTT  
53351 TCTTTTCTCT GCTTCCTTCC AGTGGCTTGC CTCCTTACCC TGGCTCACAT  
53401 CCCTGCTGTG GGAAACATCT TACAGCATAG AAGAAGGGGT GCAGGGGTAA  
53451 GTAAGGGAAG GATTGAGCAC TTGGAGTCCT CTGAGTTGGA TGGTTCAGTC  
53501 CCGAAAAGGG GGTGGTGAC TTTGGAGCAG GGGATCAAAG AGCAAGCACC  
53551 AGTGCTTGTT GCTTCTCTGG CTCCTGAACA AGCAGAACCT CCTCTCTTTC  
53601 CCTGTCCTGG ATACCCAGCG TGGGACCAGC CTTTACAGC CACCCTGTCT  
53651 TGAGTTCCTG ACTCTCCTCC TTCCCTCTTT TGAAGGCTAG AGGTGCTGGT  
53701 GTCGGCTAGC AACAGGTTGA GGGAGTGTGG CATTTCACCA GGTCTGGAGG  
53751 AGAGCGGGCA CTCAACCTGG CCCCTTCTGC GGAAAGGCCC GTAGCATCTC  
53801 TTGTCAGCCT TCAGCTGAGC TGTAGCTGGC TTAGCGGGCT CAACTTCGAT  
53851 TTGGAAGGTT GTTTTGACAG TGAGACTTCT GGATTGGCAG ACAGTAGTAT  
53901 TTGGGGACAT AATGATTGCT CTTATTGAAC ATCGGATAAG GCATTTTACA  
53951 TGTGCTCTTT CATCTACCTG TGTAAGTAG GGAATGTTTA TTGCCACTTT  
54001 ACAGATAAGG AAATTAAAGC TTGTACGTGG GGGAGCCAGG GCTTGAACCT  
54051 GATTCTGTTG GACTGCAGAG TTCCTCGGGA TCCTCCCTGG CACAGATGTC  
54101 TGGCAGTATT GGCCACTGGT CGTTTTTTGG GTAGTTCTCT TCCCCATTG  
54151 TAATAGTCTC ACCTCCTTCT TGACAATGTT GATGTTACAC TTGTTTTATT  
54201 TTGGGGCTTT TTGTGTTGT TTGTGTGTGT GTGTGTGTT TCCTTTTTGT  
54251 GAATGGGGGT CCACTGTAT TGCCTTTTTA AATATATTCT TTTTTTTTTT  
54301 TCCTTTTTGT GAACAGCAGG TCTTGAATC TTGGGCTCAA GCTATCCTCC  
54351 TGCCTCTGCC TCCCTAAGTG CTGCCTGTAA AGGCATGAGC CACTGTGCCT  
54401 GGCTTGATGA TGTTGATGAT AATAATAAAG TTAATATGTG CTGAGTAGGT  
54451 GACAGATTTA GGATTTGAAA CCTGGCAGCT TATCTCCGAC ATCTACAGTC  
54501 TTAACCAGAA AGGAAGAGAA TGAATGGTAC AATCTTGCTT GTGGTTGTTA  
54551 AGCTCCTTGA GGCCCACTTG TGCAGCAGGG CCAGGCAGGG AATGCTGACC  
54601 TGCTGTGCCA CACAGACCAG CCCCTCGGTT CACCAAGAGG GATGGGCAGA  
54651 GCAGAGCTCA GGATGGGCAT GGGATGCCCA GATTTGGTCT CAGTTGGCAA  
54701 AAGGCCCAAG TCTGCAGGTA GATGCTAAAT CCCTGGTCTG GATTTTGAGA  
54751 ACTTAGAGAC CGTCACACTT CCTGCTGCCT TGGGCTTATA TCCTCGGAGA  
54801 AACAGGGAGT GACAACAAAC TTAGAAGGTG AACTAGAGGT TGCCAAGGAA  
54851 ACTTTCCAC CCATCTTCT CTCGTAGGAG TTGGGCAGA AGGAAGGTTT  
54901 TTTCTGTTT ATTGCCGTT AGGCAGATGG GTAGGGTTGG AGGCAGTCTA  
54951 GCAGACTGA AAGGGAGGAT GGGGCTGAGA AAAAGGTAGC CTGAGGAGAC  
55001 CAGGCTTTCA GTACCCTGCT GGACAGGGCT AGGGTACCCT TCAGGAGGCT  
55051 GGCCCAATCA GGTGCCAGCA GGGCCTAGAA ATGCCCTTCT CTCCAAGGGG  
55101 TGTGAACCT AGAGTTCCTT TGGAAGGGAA AAAAGCAGGT ATTTAAAAAT  
55151 CCACTTGTCT TGCAGACACT GTTTGAGGAC CAACCAGGCT TAGGTGAGCT

FIGURE 3A-24



55201 ACAGGGTGCG TGGAGAACAG AGCACCAGAG AGCTCTGTGG GCTGGAATGA  
55251 GCAGACAATA AGAGCTGGGG GGCTTCATGG AGATGCAAAG GTTGATGAGG  
55301 AAGAGAGAAG GAAGTTAAAA GGGCCTCTTC TGGGATGTGA GGAGCCTCCC  
55351 CCTTCAAACA TCTACCAAAAT GCATGGGATC TTCCTCCTCC AAGGTCCAAC  
55401 CCCATGTGTT TCTGGGATCT GGTCAAACAG CTCACCAAAA GACAGCCTGC  
55451 AGCTACCATG CAAAGGCCCT ACGTGGGCAC AGTGAAGAAG GGGAAATGTC  
55501 AGAATCAGGA TACTGTACTT AACTTGCTGC TGTCGTTTCT GCCTGAAAAG  
55551 CATCTGGTTG AGCTAGCAAG CTTCTTGTCT AGGAATGCTG GACAGTTCCT  
55601 TGGGTAGTAG CAAGTCATTC TTTTTTCTC TGTGGTTTTT GAGTGCTTCA  
55651 CGTACAGCCA GCAGGGGCCA TGAAAGGAAG AACTTTCCT CACACTCCTC  
55701 TGGTCACCCT GCTGCCCTCC AGACTGTTTC CTTGAAGTTT CCAAGGCAGC  
55751 TCTGGATGGT TCTGGGATGA GGCTCTGGCC TCATATGCTT TGTTCAGTA  
55801 TGCTGGAGCG ATCGCTCCAG ATGTTCTTTG TGAGATGTAA ACCAGGGCGC  
55851 TAATCAGGAG TTAGACCAGA CTCTGCATTT TTTTTTTTTT TTTTTTGAGA  
55901 CAGGGTCTCG CTCTATCACC CAGGCTGGAG TACAATGGCA TGATCATGGC  
55951 TCACTGCAGC CTCGAACTCC TCCTGGGTTT AAGCGATCCT CCCGCCTCAT  
56001 CCTCCAGAGC AGCTGGGACT ATAGGTGCAT GCCACCACAC CCAGTTGATT  
56051 TCTTAATTTT TTTTTTTTTT TTTTTTTGAG ACGGAGTTTC ACTCTTGTG  
56101 CCCAGGCTGG AGTGCACTGG TGCGATCTCA GCTCACTGTA ACCTCCTCCT  
56151 CCTGGGTTCA AGCAATTCTC CTGCCTCAGC CTCCCTAGTA GCTGGGATTA  
56201 CAGGCACCTG TAATCCACCA TGCCAGCTA ATTTTTTGTA TTTTATAGTAG  
56251 AGACAAGGTT TTAATATGTT GGCCAGGCTG GTCTCGAACT CCTGACCTCA  
56301 AGCAATCCAC CTGCCTCAAC CTCCCAAGAT TTCTTAATTT CTTAATTTTT  
56351 TGTAGAGACA GAGTCTCCCT GTGTTGCCA GGCTCGTCTC AAGCTCCTGG  
56401 CCTCAAGTGA TCCTCCTGCC TCAGCCTCCT AAAGTGCTGG GATTTAGGCA  
56451 TGAGCTACCT TGCCTGGCCT AGACTCTGAA CAGTTTTAGT GAGATACCAT  
56501 AAGTTTATCC AAGTTTCTTC TGTGTTGTAG CATATATTCT TTTTACTGC  
56551 CAACCAATAT TCCCCGGTAA GGATATGCTA CGTTTGTCTA TCCGTTTCATC  
56601 CAGCTGATGG GCATTTGAAT TGTTTCCACT TTTTGACTAT TATGGATTAT  
56651 GGTGCTGTGA ACCTTGTTA CAGTTTTTTT GTGGATTCT GTTTTCATTT  
56701 CTCTTTTGTA TACTGAGG AGCGGAATTG CTGGCTCATA TAGTCTGTGT  
56751 TTAGCACTTT GAGGAATGTA CACGTCTTCA CATAGATGTA TGTTTTTTGT  
56801 CTAGACCATA CCCTTTTGT ACAGTTGAA CATCCGTAAT CAAAAGCCA  
56851 AAATGCTCCA AAATCTAAAC TTTTGTAGTG CCAGCATGAT GCCACAAGTG  
56901 GAAAATTCTA CACGTAACCC CATATGACAG GTTATAAGCA AAATTCAATC  
56951 ACTTTATTTT ATGCACAAAA TTATTTTAAA ATGTCATGAA ATTACCTTCA  
57001 GGCCATGTAT ATAATGTACA CATGAAAAAT AAATGTTTAG ACTTGGGTCC  
57051 CATCCCTGAG ATATCTGATT ATGTATATGC AAATATTCCA AAATCCAAAA  
57101 CAATTTAAAA TCTGCCACGT TTCTGGTCCT AAGCATTTTG GATAAAGGAT  
57151 ATTCAACCCG TATTATGTTT ATATGCCTCT TCAGTGCTGG TAGTTGTAGC  
57201 TTCTGCTTCC TCATCCCCTC ATTTGAGCCG GGTGGCAGAG CAGGGCAGAC  
57251 TGCTGCCTTG CTCAGACCTA ATCGTTCAGT TCTTTCATTG TACAAGTATT  
57301 CATTGAGCAG CAAACATAAG CCAGTCTCTC TAAGTGCTGG GATGTATCAG  
57351 TGAATAAAGA ATATATGCCT GCTTTCATGT GCTTCCATTT TTAAGGGGGG  
57401 AGATGGCAAA TAAATGTAAA GTGATAAATA ACAAAGGTTT AGTGGGGCAT  
57451 TCGTAGTTCA GCGGCAGAAA TTTCGTCTCC TACGCGGGAG ACTCGGGTTC

FIGURE 3A-25

57501 GACTTCGGCC ATGCAGTCCT TCCATGCAGG AAGGGCTACT ACGTTTCTAC  
57551 CCAACAAAGT TATTATGGCT GGACGCAGTG GCTCACGCCT GTAATTCCAG  
57601 CACTTTGGGA GGCCAAGGCG GGCGGATCAC CTGAGATCAG GAGTTTGAGA  
57651 CCAGCCTGAC CAACATGGAG AAACCCTATC TCTATTGAAA ATACAAAATT  
57701 AGCCAGGCGT GGTGGCGCAT GACTGTAATC CCAGCTACTC GGGAGGCTGA  
57751 GGTGGGAGAA TTGCTTGAAC CCGGGAGGTG GAGGTTGCGG TGAGCTGAGA  
57801 TCGCACCATT GCACTCCAGC CTGGGCAACA AGAGTAAAGC TCTGTCTCAA  
57851 AAAAATAAAT AAATAAAAAA TAAAGGTTCA TGTAAGTTTT GGGTGGCGAT  
57901 GAGGGCGTTG AAGCAGTTAT GACCATGTAG CTACCATGAC TTTGAGATGC  
57951 AGTCTTCTCG CAGTGTGCAC AGGCAGCATG GAGGGAGGCA GGGTACCGGC  
58001 TCTCCCTCCT GAACCAGACG AGCTGTTGTG TTGCCAATGG AGGTTCAGGG  
58051 AGCCAGTGAT GGGACAGCTC TGCTCCTGAG CTTTGCCACC CACAGGACCT  
58101 GGGCACTGGA CCTTATGATG TGCTTCTCTG GAGTGAAGAC TGGCTGTCAC  
58151 CTCAGCCCCC TCTCCTTTCT TCTGCTGCCA TATCATTCTT CACATGCCTA  
58201 CCAGCCCCCT GGAATCTGCC CCTGCACCCT CATCCCTTAT ATATTTTGCA  
58251 GAGAGCGTTT AGAGGACTGG AAGTGTGGCA TGTAATGGTA TCTCTGTTTC  
58301 CACCCCGCAG CCCACCTTGG GACACCTTGA CTCCAAGCCC AGCAGTAAGT  
58351 CCAACATGAT TCGGGGCCGC AATCAGCCA CCTCTGCTGA TGAGCAGCCC  
58401 CACATTGGAA ACTACCGGCT CCTCAAGACC ATTGGCAAGG GTAATTTTGC  
58451 CAAGGTGAAG TTGGCCCGAC ACATCCTGAC TGGGAAAGAG GTGAGCACTG  
58501 GGA CTGGGGA CATGGCAGCA CCTCCCAGCC CTGTTGACAC TCCAGCAGGT  
58551 GGTGATGGGA CTACTACTGC AGCCAACCTC TTGTTTATCC GGCAGAAATG  
58601 AGATCTGAGA TATAGGGGTG CAAAAAGCTG TGGGATGAAA AGGAGTAAGA  
58651 AATATAAAGG AGGAAGTAGA TTGGAATCCT GGGTTTCGCT GGTGAGAGAA  
58701 GTGATTTGGG GCCTTTTGT CTCATCCTCA GGTAGCTGTG AAGATCATTG  
58751 ACAAGACTCA ACTGAACTCC TCCAGCCTCC AGAAAGTAAG CACATGGCAC  
58801 CTCCTGTCCC TTTTTTTTTT TTTTTTTTTT TTTTTTTGAG TCAGAGCCTC  
58851 ACTCTTGTCG CCCAGGCTGG AGTGCAATGG TGTGATCTCG GCTCACTGCA  
58901 ACCTCCGCCT TTTGGTTTCA AGCGATTCTC CCGCCTCAGC CTCCCCGAGTA  
58951 GCTGGGATTA TAGGCACCCG CCACCACACC TGGCTAAGTT TTGTATTTTT  
59001 AGTAGAGATG GGGTTTCACC ATGGTAGCCA GGCTGGTCTC GAACTCCTGA  
59051 CCTCAAGTGA TCCGCTCGCC TCGGCCTCCC AAAGTGCTAG GATTATAGGC  
59101 GTGAACCACT GCCCCCAGCC CACCTGTCCC TTTCTAAATC TCTCTTCTGG  
59151 GGTCATGAT CTACTGACCC CATTTAGACC TTCTCTTGAA TTCCTAGTTT  
59201 AAATTTTCTG GCCATTTTCG TCACCGTCCC CCAACCATTC CCTCCCATGG  
59251 CTCTGCTACC TTCGGGGCTT TGGTTGGATC ATCTGTGGTG ACTCCTCCTG  
59301 AGTGGGCTTC CTGGCCATAG GCACTGGCTC TTGTGAAGTC TTTCTGTTCA  
59351 TTCCCAGCCA CTTGGCCTAC CTGTCTGACC TACTTCCTGC ATCTTGTTAT  
59401 CTTCTGGCTT GTGGCCAGCC CTATGCAAAA ACACATGTTT GTAGCCACTA  
59451 CTAGAAACAC GTGCAGCTAC TTCAAGATCT GGAATGATAC AGGGGAGTGG  
59501 CTTTAGAAAT ACAAGAATAA GAGGAAGCAG GGAACCTGCC GGTGGGTTCT  
59551 GTGCCAGCTA CCTTTTAGAG AATGAGCTCC AGCTCAAATT TTCTGAACAA  
59601 AACCTAGTTC TGTTTCATCT GTGGCAAATC AGATATTTTC TCCATAAGCA  
59651 TATTGTGGCA GTTGAGTTAG GAGAAGGCAT GATTCGTGCT AACAGAGTCA  
59701 GATAGTGATA CTGGGAACCT TAGGAGTAAG GGCTGAGGAT TGTTGTTGAG  
59751 GGCGATGCTC ATGGAATTAG AGTGGATGAG TTGTTCTCCG GACATGCAAA

FIGURE 3A-26

59801 TAGCCAGAAC CAAGGTGTTT CCTATTTATT GTTACCCCTG GGATCCCTTC  
59851 AAGGGTTCTT CAGTTCAGTA GAAACATTGT TGTCATCATC AGGGTGTCTC  
59901 TGCTTGAAGC TTTCCAGGAG GAAGGGAAAA AGGGCTGCTT ATGACATCCT  
59951 GGCTCCAGCC CCACAGAAGA AGTCAGCGTG GGGTAGGCCA TTTGGCCTTG  
60001 GGAGCAGTCT AGCCTGCCAT CGTAATAATC GCCAGTCCAC CAAGCCATCT  
60051 TATTCCTGAC CTTGTTTTTC TCCCTAATTC TTCTTGGTTT TCTCCCTAAT  
60101 TCTTCCTGAC TCTCTGGAAG GCACCAACAC CAGACAAATA GAGCCATTTT  
60151 CAAAACCTTT TGAGACTCTT TGTTACTAAA GCCAGTCTGA TTCTGGCCAA  
60201 AAATGTGATC TCAGCAATGA TCCCTGAAAA ATGAACATTG AAGAAGCTAG  
60251 CCCCCTCAGG GGTCTAGACA AGCCCAGAAA ACCCCAAGTT CTCCCAGAAG  
60301 AATGTCACCT CCATGCCAGG TGAGCAGCCT CAGGGGAAGA AGCCCTGGCA  
60351 GCTGCCTCTG GCCCTATTTC AGAGCTGCTC CCCATTACTG CCCCAGAGGG  
60401 TGGTATCCAG GCTTTTTGCC TCTCCATCCA AAATATCTGT TGGACCAGGG  
60451 AAAAAAGTAA GAAAAACCTA GGCCCTAATA AAGGGTAAGG TCAGCATTGG  
60501 GTTCCTGAGG ATTGGAAAGC CTTTTTCTTC TTTTCTTTTC TAGCTTAGGA  
60551 AAGCTCTGGG GCATCATTAAG AGGGGAAACA AATGTATTCA CTTTATTCCA  
60601 TAAACCATAT CTTGAATTAG GGCTTCCCCT AGCCCCAACA AAAACAACAA  
60651 CAAAACTAG TTCTGTTCTT TGTGCAAGTG ATGAGGCCTG AAATTACAAA  
60701 AAGCCCCACC TCCAGTTCTC TGGCCCCCGC AGAGGGGAAG GAGTTCATTT  
60751 CTGTCATCTT TCTTTATGGA AATACATGGT TTGGAGCCCC TGGTTTTGTT  
60801 TCACAAAGAG AGCGTGAGTG TGTGGAGGTG GATTTGATTA AAATTGGCAT  
60851 CAGCTATATA TAGGAGTGGC TTCTTCTGTC ACCACCCTAG AGGCCAGGA  
60901 AGGAAAGGCC TATCCCCTAG AACAGAGCCC TCTGACTACT GTAAATCAGA  
60951 AAATGATGGG GTCCCCCTCT GGTGCTCTAC CACCCTTTA CACAGACCAA  
61001 GCTGGGGTGT GTACTGTCAC TGAACCAAGG CAGCAGCTCG GATTCTGAAT  
61051 ATTCACGCAC ACGGGCTCAC ACTCCCTCCA GTAGAGGCAC CCAGCCAAAA  
61101 CCTGCCTGCT GTTTTGGGGC TGGATTTGGT AGACGCAGCA GAGGGCATGG  
61151 CTGGCTCATC CTGATGCCAT CCCGGGTAGC ACGTCCCCAC AGCCAGCCCT  
61201 CCTCCAGCTT CCCCAACTTC CCAGCCACAG GGAAGGCCGT GCATGAGCTA  
61251 GACAACCACC CTATTTTCTT TTCCCTGCCC GGTTTTGGTT TTTTGGGAAA  
61301 AACAAATCCT GGCAGGGACT GTTTGGAGAG ACCTGATGGG AGCAAGTTGG  
61351 GCAGGCATGA CCCCTGGTAT TTTATCTTCC AGCTATTCCG CGAAGTAAGA  
61401 ATAATGAAGG TTTTGAATCA TCCCAACATA GGTGAGCACA AGTTGTTATT  
61451 TCTTTCTTCT TCCCCAACAG CAAGGCACTG CTTTCCAGCA TGTCATCTTC  
61501 TCCCCGAGGT GCACTGCCTT CTGGAGTCTG CAGTCTTCAA GGATACCCCT  
61551 GGGGAAGCTC AGCTCAAAAT CCATCTCCCC TTCTGGCACA CTGGGCTGTC  
61601 TTTAGCAGTT TGGCTGGCAT GAGAGGAAT TGTTCTTGGG AGTGGGGGAT  
61651 CATGAAAGGA GGGGAGACTT TCGTTCCTAG GATGCTCCTG GACATGTTGG  
61701 AGAGCAGTAT GTGGCCCTG TTGCTTCTTG ACTTAAGGCT TGGCCTTTTC  
61751 TCTTGTAGTT AAATTATTTG AAGTGATTGA GACTGAGAAA ACGCTCTACC  
61801 TTGTCATGGA GTACGCTAGT GGCGGTAGGT GTGGAAGTGC CTCTTCCTGT  
61851 TGTGCCCCCA CTTCTTCCAC CTCCAGCCAG CTCTGACTGA GATCCCTGCC  
61901 TGGTCTCTTA CAGGAGAGGT ATTTGATTAC CTAGTGGCTC ATGGCAGGAT  
61951 GAAAGAAAAA GAGGCTCGAG CCAAATTCCG CCAGGTAGGT GTGACTCCCT  
62001 CCATAGGAGC TAGGCCTGAC CTCTGCTTTT GGGGTTTGAC ATGTAAGGAT  
62051 AAGCTGCCTG TCTGTAAGTG GCCCTTGGAG GGTACTTTGG GCTCTGCTTA

FIGURE 3A-27

62101 TCCGTGTGGC AGGTTAGCAC TAAGTCACAG GGTCAGTCT CTGTCAGCCC  
62151 CTGTGGCCCA CCCTCAGGCA CCCCTGGGTT AACCCCTTCTT CCTTCCTTTC  
62201 AGATAGTGTC TGCTGTGCAG TACTGTCACC AGAAGTTTAT TGTCCATAGA  
62251 GACTTAAAGG TAAGGCATGC ACTTCTCCTT GTGCCTTTGA GTGGGAGCCA  
62301 GGTTGTTGCC TCTTGTTCT CCATGATAAA ACCATCAATA ACCATCAGGC  
62351 CCTGAGTGTT CCAGGAACT CCAGCCTTTC TTTTTTCTT TCTTCTTTC  
62401 TTTTTTTTTT TTTGAGATGA CCAGAAAGCC CCTAGGGCTG CCTCTGATAG  
62451 AGGCCTTG TG GCTGGACCTC GGGTTCCATT CTAGCCCTTG AGCAGGGGCC  
62501 CTCTGCCATT TCACCTCTTG GCACATCACC TTTTAGTGCT GCCAAGCAAG  
62551 GCAGGCACAC TCCAGGCTTT CTCAGTCTTT CAGGCAACCT GGTAGCTGAC  
62601 CCAGGGAAGA GTGCTGAAAG TTCCACAGCT GTATCCCAGC TGCTTTGCAG  
62651 GCAGGCACAC ACATACCATC TCCATCACC AGATACTCAA GTTTGAGGAC  
62701 ACCTGTGGGT CTCTTGCTG CTGAGTCCTC ACAGACATGA TTTGATTAAC  
62751 CTGGGCCTGA TGCTGAAGCT TTGCACAGCT CACAGGGTCT CTGGGCCTTC  
62801 AGATCCCATC TCTCCCATGG CTGCCCACGT GAGGAGTGGC CTGCATTGCC  
62851 TTCCTCCTGC CCAGCCTATT CACGCTGATT GAAGCCCTGC CCTGAAATTG  
62901 GTGGAGAAAG TTCTGAGACT GAAGATGACT TTCCGTTTGT TCTCCCATTC  
62951 CCCTCAGCTC CTTCTGCCC AGGGCCTTAG TCTGGTCCAC TTGGTTCCCT  
63001 GATGTTTTCC ATCTTACCTC CCAGGCAGAA AACCTGCTCT TGGATGCTGA  
63051 TATGAACATC AAGATTGCAG ACTTTGGCTT CAGCAATGAA TTCACCTTGT  
63101 GGAACAAGCT GGACACCTTC TGTGGCAGTC CCCCTTATGC TGCCCCAGAA  
63151 CTCTTCCAGG GCAAAAAATA TGATGGACCC GAGGTGGATG TGTGGAGCCT  
63201 AGGAGTTATC CTCTATACAC TGGTCAGCGG ATCCCTGCCT TTTGATGGAC  
63251 AGAACCTCAA GGTGGAGTGA AGTGCAAGCT TTTTATTGCT TCTCATTTCC  
63301 TCTCGGCCTC TGGTCTTAGC CCTGACCTCC TGCCTTTGCC ACCTGTCTAC  
63351 ATTTGTCCCA AGCCAAAGCT TCAGAGAAGG GCTTGCTGAG GTAGCAGCAG  
63401 TCAAAGGCCT TCTGCACCTG GGAATGAATA ACCTCAGTTC CTTTCTCGAA  
63451 AGATGGGATA AACTGTGTGT GTGTTTATCC CCCAAGGCAC TCCGGATTGC  
63501 AGGCCTCGGA CTGGTCAAGT TAGAGGGTAC GAGGGTATTT GACTTCACTT  
63551 GCCTCTCTGG TGAGGTGTCT TGTCCCCAGG CTGTCTGCCT TCTTCCATAT  
63601 TTCATTTATG TCTGCTTTGC CAGGCTTAAG CTCTCAGGAT CTTGGATATT  
63651 AGGTTTCTTC CTTTGGCCTT GGGGTGATTT CAATTTTCTA ACCCTGGATC  
63701 CTCCTGCAGG AGCTGCGGGA ACGGGTACTG AGGGGAAAT ACCGTATTCC  
63751 ATTCTACATG TCCACGGA CTGAAAACCT GCTTAAGAAA TTTCTCATTC  
63801 TTAATCCAG CAAGAGAGGC ACTTTAGAGG TGAGCAGTGG AGCCCAACTG  
63851 GCGGAAGGGC CTGGGGTCCC CACAGAACT TTCCAGCTGA GTTTCTTCCC  
63901 CCTGCCCTTT TCCTTCTCTG TGCTCCCCAG CAAATCATGA AAGATCGATG  
63951 GATGAATGTG GGTCACGAAG ATGATGAACT AAAGCCTTAC GTGGAGCCAC  
64001 TCCCTGACTA CAAGGACCCC CGGCGGACAG GTGAGGCTGT GCCGGGCTGT  
64051 GAGGTTAAGC TTGCCTAGGA GTTGAGGCCA GTCTTAAGT TATGTCCCCC  
64101 TGTGCAGAGC TGATGGTGTC CATGGGTAT ACACGGGAAG AGATCCAGGA  
64151 CTCGCTGGTG GGCCAGAGAT ACAACGAGGT GATGGCCACC TATCTGCTCC  
64201 TGGGCTACAA GAGCTCCGAG GTGTGTGCTC CCCGCTCCAT TCTCTGACCT  
64251 GGCCAGCCTC ACTGTCTGTA GCACCTATGC TTCTAACACC TGTTGAGGGC  
64301 AGAAGCTCAT CTCTGAGTAG GTGTGCTCTC TGCTACCAA TTTTAAGCCT  
64351 CAGCTTTGGT GTCTAAGGTC CTCTGGCCA TTAAGTATC TCCATGAGTG

FIGURE 3A-28

64401 AATTAATAGA AAGCTGGTAG GGTCCGTGTG GGA CTGGGTC AGAGTTTCAA  
64451 TACGGGTGAG TTGATCTAGG TTAGTCTGCA TTGATTAGAT GTGTCTAGGT  
64501 CATCGGCTAG CACTACTACA TTGATCTAGA TATCTTTGTG TCTCTTTTGT  
64551 TATCTGGAAG TGTACATTTT TGGGTGTGTG TGTGTGTCTC TGTGTGTGTC  
64601 TGATCGGAAG TTTGAGTCTG TTGCTTTTTT TTTTTTTTTT TTTTTTTTTT  
64651 GAGACGGAAT TTCGCTCTTG TTGCCCAGGC TGGAGTGCAA TGGCAGGATC  
64701 TTGGCTCACT GCAACCTCCG CCTCCCGGGT TCAAGCGATT CTCCTGCCTC  
64751 AGCCTCCCAA GTAGCTGGGA TTACAGGCAT GTGCCACCAT ACCCGGCTAT  
64801 TGAGTCTGTT GCTTCTGTCT AGTGCTTTAT GTTTGGGTGT GTGTATCTGT  
64851 GTGTGTGTGT GTGTGTGTGT GTGTGTGTAT GTGTCCGTCT TCCCGTCTGT  
64901 GGATCTGGAG ACTTTGTGAT TGTTCTTCTG CCCATTTGGG TTTTGTTCAT  
64951 CATCTGAGTA TCCCCACATG AACTCCCAGC CTCCCTGCCC TGCTCTCCCT  
65001 CTGGTGGTGG GATCCTTAAG AGGCACCTGG TGACACTTGG TATAGGCCCA  
65051 TATTGCTCTG TGTTGAGGGG AGTGGACTTG AGTCTGGACA TGTGTTCTTG  
65101 CGGATGTTTG TGTCTCTGGG TGTGTGGGCT TATGTATTCC TTTCTGAGAC  
65151 TGTGTTTGTG AGTGTCTGTG TCAGAGCATG TGTGTCTCCA GGGTCTCCTC  
65201 CAGGGGGGAT GTATTGGTCT TACAAGTGGA TGTCCGGTAT GATCCTGGGG  
65251 TGTTTGAGTG TTGGGAGAGG GCGGTATGTG TAAATGTGTC CATCCATAGG  
65301 GATCTCCACA TGA CTCTGC CCTCCCTTGA AGCTGTTTTC TGTTCCTTTC  
65351 AGCTGGAAGG CGACACCATC ACCCTGAAAC CCCGGCCTTC AGCTGATCTG  
65401 ACCAATAGCA GCGCCCCATC CCCATCCCAC AAGGTACAGC GCAGCGTGTG  
65451 GGCCAATCCC AAGCAGCGGC GCTTCAGCGA CCAGGGTAAA TGCTTTTGGG  
65501 AGTTGTAGGT GGGGACTCAC CCCTCTCCAG AGAGGTTACA GTTCTGTGG  
65551 GGACTTGGGT AACACAATA AGTTTCAGTC CTGGTTCAGC CACTTATTAG  
65601 TAGTGTGGCT ATGGGCAAGC CACTTCCCTT CCCTCGCCTC TGTGGAATGG  
65651 GGGCTTGCTG GGTTGTTGGC CAGCCCTGTA GGAAATGAGC ATGCGTGGGG  
65701 CTGGCACTCA GTGGACCCCT TGGCCTTACC CATTCCCAC CTCCCTCTGG  
65751 CCCAGCAGCT GGTCTGCCA TTCCACCTC TAATTCTTAC TCTAAGAAGA  
65801 CTCAGAGTAA CAACGCAGAA AATAAGCGGC CTGAGGAGGA CCGGGAGTCA  
65851 GGGCGGAAAG CCAGCAGCAC AGCCAAGGTG CCTGCCAGCC CCCTGCCCCG  
65901 TCTGGAGAGG AAGAAGACCA CCCCAACCCC CTCCACGGTG AGCCGCACCC  
65951 CCCGCTCTCT CCTTCCTTCC TGCGGTGGGG CCTGCCCTCT CCAGGCAGCT  
66001 CTTCTCTTAA TTCAGACTCT GTTCCCTTTG GCTACTACTT CTGCTTATAG  
66051 CAGGAAGCCT CGCTCCAGC AGTAAATGCA GAATCCTTTC CTTAACCTAC  
66101 CACTGTCTGC TTCAGGTGGA AGGGACAGGA AGCCTGTTCC ATGAACCTGG  
66151 GGGGAGAACC TGGCTGTAGA CCACTTTGGC TTTCTGATAG AACGCTTGCC  
66201 CTTTATTCCC CACAGAACAG CGTCCTCTCC ACCAGCACA ATCGAAGCAG  
66251 GAATTCCTCA CTTTGGAGC GGGCCAGCCT CGGCCAGGCC TCCATCCAGA  
66301 ATGGCAAAGA CAGGTGAGAG ACCCGGGCCC TGCCTGCCTC ACTCCCTAGG  
66351 AGCCATGTCT CACAGGGTGA TGTCTGTCAG CAGCACCGTC TCCTGTCCCT  
66401 GCCAGCGCAT TGCTCCCTGC TCCCTGGAGT TCCATCCTGG CTGTGTCCAG  
66451 TCCAGCTTTC CCCTCCCCTA TTCCACGCCA TTGCCTCCTC CCCATCTTCC  
66501 TCTGACTGCT ACTTGAGT TGGCAAGTGT GGGGCTGACC GTGGCCATCT  
66551 CAGCTACATG CTCGCTTCTT GACCACGGCC AGGGCATGGC AGCTGCCCTC  
66601 CTCTAGACAT GAGCAGCTAA GGCCTTGTGT TGGGGGTCCC AGCTCAGGGC  
66651 AGAACCAAGA GATGCCACC TTGAGGGGTG TACACATAGA GGGCGACTCC

FIGURE 3A-29

66701 AGCCATCCCC ATGAGACCAG AGCTCCCCAG CCTTCACCGG CCGCATTTCT  
66751 TGGTGTGCA TTCCTGGCTC TATCTCTTCT GAGTTTATGA AAGTTTCCCC  
66801 TCAGCAACAC CCCACTCTTT CTGTAGAAGA AACTCTCCTG TTCTTAAAT  
66851 TCTTAGGAGG CCAGTGCAGC CTGGAGGCAG CGGCCCTTG TCTGCTCTCC  
66901 TTCATTTCTG ATTCTCTTTC CCAGGCACTG ACCCACCTCG CTGCTTCCCG  
66951 ACCTCACTCA CCTCCACTTC TCAGCCCCGC ATTCTCAGT TCTGACTTGC  
67001 ATCCCCGCTG TGCCAGGCC TGACTTCTAC CCTGCCAGAG CTCCCCAGCT  
67051 CTGGCCCTTC CCCTGCCCTT GCTTCCTAAT CCAGGCCTCC CGCCCTCACT  
67101 CACCCCTAAC ACGGGCCTCT CCGCTGCTTT TGTTTCCTAG CCTAACCATG  
67151 CCAGGGTCCC GGGCCTCCAC GGCTTCTGCT TCTGCCGAG TCTCTGCGGC  
67201 CCGGCCCCGC CAGCACCAGA AATCCATGTC GGCCTCCGTG CACCCCAACA  
67251 AGGCCTCTGG GCTGCCCCC ACGGAGAGTA ACTGTGAGGT GCCGCGGGCC  
67301 AGGCAAGTGT GCTGGGGCAG CTGGTGCACC TGCTGCCCTC AGCCCACCCT  
67351 ACCCCCTTGC CCAACAATT TCTTCTTCCC ACTTGGGGGT CCTGCTGTGT  
67401 TCTTGTATC TTAGCCACAA GAAATGGGTC TGTCCCTGC GGCCAGGAAG  
67451 TGGAGGGAAC AAAAAAGAGC ATTAATGCCC CTCTTTTCCA GTTCTCCCTC  
67501 TCAGAACAGG TATGCAGGAA GCTGTCCTAA GGCTCCAAAG GGAAACCTTT  
67551 TTGTTCTGAA CTTCCAGGG TTTCCTTAGG GACCCCGGG ATAGTCGGCA  
67601 TCACAGGGAC TCAATCCTCA AGGGTTGGTC CCCATTGCCG CTTGAGGGT  
67651 CCAGTCTGCC CGGCTCCCAG GGAGCCCGCT GTCTCCAGCC TAAACCACAC  
67701 TCCACACAGG GGTCTTCTC TGCCTCCCTC CCTCCCTTCC CAAACCATCT  
67751 CTTTCCACTT CCACGAGACT TCCTTCTCAC CACTGTCCTC AGTAGTCACA  
67801 CCCTTCCTTC TGTGTCCTCG TGATGGCTGC CTCTGCCCTA GCATCCCCCT  
67851 CCCTGTCCCC ACCACAGGGT GTCCAGGTGC CCAGTGATGG CTGTCTGTGA  
67901 CCCTAATTG TCCCCCTCAA CCCACTTCT CTTCCACAG CACAGCCCCC  
67951 CAGCGTGTCC CTGTTGCCCTC CCCATCCGCC CACAACATCA GCAGCAGTGG  
68001 TGGAGCCCCA GACCGAACTA ACTTCCCCCG GGGTGTGTCC AGCCGAAGCA  
68051 CTTTCCATGC TGGGCAGCTC CGACAGGTGC GGGACCAGCA GAATTTGCC  
68101 TACGGTGTGA CCCCAGCCTC TCCCTCTGGC CACAGCCAGG GCCGGCGGGG  
68151 GGCCTCTGGG AGCATCTTCA GCAAGTTCAC CTCCAAGTTT GTACGCAGGT  
68201 AAGCAAGGAG CTTTGGGTGG CAGAGAGGCT CAGGCCAGGC CTTCTGTCTT  
68251 TACTCGGGGT GGGTTGGGGT TTGGGGGTTG GGGTTTGGGA CACTCTGTAC  
68301 CGGTATTGGG TCCTGGGGTT AGAAGAGGCT TCAGGAAGCA CAAGAAATTA  
68351 GGTCTTTGTC AACACCTTAT GTGCCAGGC CCACCCCTCT TAGGCCTCTC  
68401 CCCAACTCCT CACAGGCACC CCTCATTCTC TGGCCCCAAG CAGATGGCCG  
68451 ATGCCGCCTC CTCTCTAGGA GAGTGTGAAC TCAGATGCTA AAATAAAAGC  
68501 CCCCCCTTCT CTCCTGGGT CCCATGGAAA CTTATATTTG GTGACGCAGC  
68551 TGCAAAGTCA TGAGGCATGA GCCAGGCTGG GGCCAGCAAG GAAAATTTTG  
68601 TCCTGGTCTC TTGCCCTTT GACTGCCTCT CCCACTAGTT GGTCTGTCTT  
68651 CTGGCTGCAG GCGCAGCCAT GCCCTTCTGC CCGGGGGTTT TAGGGTGAAA  
68701 CCTATAAATG AAATCACTGG CGAGGGCCTA CAGTGGCCTC TTCCCTAACC  
68751 TAACTCCGAT GTGCCAAAGG TTTCTGTGT TGGACCCAGG GTGGGGATCT  
68801 CTTACGGGG TTTCTCACAC CTGAGCCCC AGCCACCACA GAGGTGCAGC  
68851 TTGAAGTGCA TCCAGCCAAC TGGCTGGCCT CCTGGGATGC TCCGCATCCC  
68901 CATCCTGCCA TTCCTCTCCC TGCCTTGGAG TAGCAGCTCA GGAAGCAGCA  
68951 GGGGCTTTGA GAGAACAGGC TCGCCTGCC TTCTCTACG TTTCACTCCA

FIGURE 3A-30

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69001 CTCTGCTGGA GGAGCCAAAG CCACTGCCCC ATCCGAGCCC CAGAATGCAA
69051 GTGTGAGGCC TGCAGAGAGT GTGGGCAGGT CTGAAAGCCT GGGACTCTAG
69101 TCTCGCTGAG CGGCTCTTCC GAAAATGGGA TGACCCTTGA ACCTGTAAAG
69151 CCACCTCCCC CACCTGCTTA TCCACATACC GTCTTGTTGG TTTTTTTTTT
69201 ATTTCTTTTT TTATTTTGTG TTTTTTTTGT TTGTTTTTTT AGAAATCTGT
69251 CTTTCAGGTT TGCCAGAAGG TAGGCGTTGA GCCCGCTGTG TGTGTGTGTG
69301 TGTGTGTGTG TGTCTGTGTC CTGTGTCCTG CCTCCATCAC TAACTCCCCT
69351 TTTCTGGCTC TTA CTCTCCT CCATCTGCTT AACCAAGTCT GTGTGGCCCT
69401 CCTCTCTCTG CCATCTTAAA GGGATGAAGA CTGCCTCTGA TTGGGCATCA
69451 GCACAAGGCC TGCCCTCCGT GCCCCAGTA CAAACAGGCA GGGCTAAGAG
69501 GCCACATTGG CCCACTCAGG GCAAATGGCT TTAAAAATGA GGGCCTTCCT
69551 TGGGCCCACA GTTAACGCCT GTCCTCAAGT AAGGGGAGAC TGTCTCAGGG
69601 AAGCCTCCCT TTAAGATTGT CTCCTCTCAC CCACCCACC CCACCCACC
69651 TCCCTCTCAC CCCAGGTTT GGTCAAGT GTTGGGATCC TTTCTGCCC
69701 TTTCCCTTGT CATGTGCATG CGCTATGAGG AAGCTCCAGG GTTACAAGTG
69751 CATCTGGGAT GGTATCTTGT TTGTTGTCTC CTGGGTTTCC TGAAGTTCAG
69801 AGCTATGTGA CCTCTTCCCC GTGGCCTATG GGATCGCAGG ACTTTGGAGA
69851 CACTACGGGG ACCCTGGGGC CCAAAGTTT CAGTCTGGCT CCCCAGACC
69901 TTAGGAGCTT TTGTCTCACA AATGGAGCAC AGCACCCCT CCTGGCAGCT
69951 CCTGCAGAAC TAGCCCCACC CACCCGCACC CCTGCCCCAG CACCCTGCC
70001 ACCAGCAGCA TCTGGATAAA TCAAGCCTCT TCTCCTCTAG GCTGTTTTCT
70051 CCAGATATGG CCTGTCTCTT CCAAAGTGCG GGGAGCTGGG ACATTCTAGG
70101 GCAACGGCCA TTCTACCCA AGCCGTAGCA AAACAACAGG AGATCTCTGC
70151 ACCCTTACTC AGGGGTCTCC CTTACAGTC CCCTTCCTGG CTCTTTCACC
70201 CCTGGCCTTA TGCTCATCCT CTCTGCAGG CTCGGGGACC AAATACCAAG
70251 CTGAAGACCA AGGGCCAGGT TAAGAGTGCT TGTTCCCCAA GGCTGTCTGC
70301 TCAGGCCCTG CATTGGGACT GGGATGCCTG GCAGGCACAT TGGTGCCACA
70351 GCTGATGGAG GAACGTCCAG ACAGGTCTT CAGGCTTTCC CTATCCCCTC
70401 CTCCTCCCAC CCAGCTGTTG ACTGCATGAC TGGCTGCTGC CTCAAGGGGC
70451 CCCAGCAGGG GGCTGCCCCA CAGGGGTCT GGAGAGAGCA GGGAGGGTGC
70501 CTTCTCGCA CAGCCGGGCT CCCTGCTCGC AGTGCGCTTG TGTGCACCCC
70551 TGTGTTGGTT GTGTCTTCCT GTTTATTTCT ATGTGCTGCT GCTCTTCCTC
70601 CTTCTCTCA CATCTTCCT CCTCTGCAAT CCCAGTTTC CTAGCTCCAG
70651 ACACCCATCT TCCAGCCAGG AGCTGGAGAA GCCGCTCAGC GGGGCCAGAC
70701 CTCTTCCCCA CCCACCCAAC CAAGGTGTCT GCCCTGCCCT GCCCCACCCC
70751 ACCCTCATCC TCCCTGCGTA TGAGCAGATG GCCTGGCAGG CCAGCAGGTA
70801 GGGGAGTTGG GAAAGGTCGG AGGAGGCCGC CTTTCCACT CAGCAGCAGG
70851 AAGCCATCCC CAGGTGCCTA CCATGCAGAC CCAGGCCTTG GCACTTTGAG
70901 TCTCTGACA GGCCCTTGCG TAGCCACGGC CCCTCCTCCT ACAGAGATTC
70951 AAAGCATTGC AGCCCTTTC CTCCAAAAGG ACTGCAGTCC TGAGACCCTA
71001 GCGTGTGGCT CAAAAACGC ACTCACACCT GCAACCCCCA GAACAGCGCG
71051 TGAGCCCTGG CTGTGGGGA GCAGCTCGT GCCGGGCCGT GTGCTCAGTG
71101 TGCTCAGTGA AGTGC GTGCA CAGCCACTCC CCCTCCTCCC CCAGAGCAGA
71151 GGCTCCTTCT CCCC GG CACA GATCTGGGAA TGTGGGGAGG GACAAGCCCC
71201 ATGTGCTGGG CTCCCTGCTG GAAAGGAATG GTTGAGCCGC CAGTGTGAGG
71251 TGCTGCAGAG CCCTGTTGGC TTGCCAGGTG ATGGGCAGAG GGCCCTGGGC

```

FIGURE 3A-31



71301 TTGGGTCCTG CCCACCCACT GGTGGCACCT CCCCAGACCC ACTCTCATCT  
71351 GGGTCTGTGG CGGCGGAAGG AGCGAGAGAT CCCAGCACTA AACTCTCCCT  
71401 CGCTCTGTTT TTTGAGGAAC CTGAATGAAC CTGAAAGCAA AGACCGAGTG  
71451 GAGACGCTCA GGTGAGAGGG CTGGAGCCAG CACTGGCCCT GCCCGGGCCA  
71501 CCGGGCTTGC CACAGCCTCC TGCTCCTCTC TTCCTTCTGC CACTTGGCTC  
71551 TTCCTCCCGT GGTCTGCCC TGTCCTACC CTCTGGGGCC TCCCTTTCCT  
71601 CAGAGAGTTT CCCCTTCCCA AACCCAATTG CAGGAGTTAC GGGCCCTTCT  
71651 CCTCAGGTCT GGTATATTCT GGAAGTCGGA GTTCTGGGTC GGGTGGTTGG  
71701 GGCTACAGAT TCCTACCCCT GGAATATCCC ACCTCCCTGT GCTCGGAGGC  
71751 TGCTTTCTGG AGAGAGAGTC TGTGCTCGTG CTGTTGAGGG CACTGGTGTC  
71801 TTCCCTGACC CCACCCCGCC TACCCCAAGG CTGGCTTCTC CTCCCCTTCG  
71851 CTGCTCTGAG AGATGGGGGT TGGAGGACTG CCACCCTCCG CCCC CGCAGG  
71901 CCAGGGGGCA CGCCTGGCTG CTCCTGCTCC CTCCCGCTCT CCTCTCTGGG  
71951 CTCAGGGGCT GTCTGCCAGG GTGGCTCTCC TGGGGTGGGG TGCCTCAGCC  
72001 CCCCCTGAC GCCCGCCTCT GCCCTCTCCA CAGACCTCAC GTGGTGGGCA  
72051 GTGGCGGCAA CGACAAAGAA AAGGAAGAAT TTCGGGAGGC CAAGCCCCGC  
72101 TCCCTCCGCT TCACGTGGAG TATGAAGACC ACGAGCTCCA TGGAGCCCAA  
72151 CGAGATGATG CGGGAGATCC GCAAGGTGCT GGACGCGAAC AGCTGCCAGA  
72201 GCGAGCTGCA TGAGAAGTAC ATGCTGCTGT GCATGCACGG CACGCCGGGC  
72251 CACGAGGACT TCGTGCAGTG GGAGATGGAG GTGTGCAAAC TGCCGCGGCT  
72301 CTCTCTCAAC GGGGTTCGAT TTAAGCGGAT ATCGGGCACC TCCATGGCCT  
72351 TCAAAAACAT TGCCTCCAAA ATAGCCAACG AGCTGAAGCT TTAACAGGCT  
72401 GCCAGGAGCG GGGGCGGCGG GGGCGGGCCA GCTGGACGGG CTGCCGGCCG  
72451 CTGCGCCGCC CCACCTGGGC GAGACTGCAG CGATGGATTG GTGTGTCTCC  
72501 CCTGCTGGCA CTTCTCCCT CCCTGGCCCT TCTCAGTTTT CTCTTACATG  
72551 TTTGTGGGGG GTGGGAGATT GTTCTCCAGC ACCCCACATT CACCCCTGCC  
72601 CAGAGATTCC CCCTTCTCCT CTCCCCTACT GGAGGCAAAG GAAGGGGAGG  
72651 GTGGATGGGG GGGCAGGGCT CCCCCTCGGT ACTGCGGTTG CACAGAGTAT  
72701 TTCGCCTAAA CCAAGAAATT TTTTATTACC AAAAAGAAAA AAGAAAAAAA  
72751 AAATCCCAGC GGCCACCTTT CCTCCCTGCC CCATTGGGAC AGTCGAGACT  
72801 GGATCTGTGG GGTTCCTCCG GAGGGTGGCT CAGGGCTGGA AACTCTCAG  
72851 GCAAGAGTGG TGGAGCTCCC GTCAGGCCCT CCGCCAGGCC CACTGTGGGC  
72901 TTCTCCCCTC TCCTCCCTCC TTCCCCTCCA AGCAAACCAC CAGAGGTGGC  
72951 CTTCCCCTGA CCTCAGGCCC CTGGGCTGGA GGCCTGGGCG GTGGGGCAGG  
73001 GGGCGGGGGT GCTGCGCAGC CCTGCAGTGG GTGGGGCTGG GGGCTGCTCC  
73051 GGGGCTGCTG AGGCTGGAGG GCCGGCACAA GGCTCCGCT CCCTCCACAC  
73101 TGTACCCTCT GCCCTCCTC CCCAGAGCTG GGCATTTCT TCCACAAGCT  
73151 GCTGTGGGGA CGTGTGTTCC CTCAAAGTCT GTGCCATCTT CTCCCACCCC  
73201 TCCCGGGTAG AAGGAGGGGC TGACCCAGG GCTGGGAGAG GGGAGGGGAC  
73251 TGGAGGGCAG ACTGGCTTCT CGGTCCCCAG GGGGCCGCTT GGGCTGTTGG  
73301 TCTCCAGAGC AGGGCCACTG GGCACCTGTG GATGGGGGAG CCTTTGTCTG  
73351 AAAGCACAGC CCCCTCGCCC TTCCTCTCCC CATGGCTTCC CTTTATTGG  
73401 CATTAACTG GGCACCAGCT CTCTCCATAG CAGTGAATTC CTCACCACT  
73451 CTCATCTCTC AGCCTTGCTT TTTCTTCTG AACTGTCTGC CCCCTCCTCT  
73501 CAGGAGACAC TGCCGAGGGC CACCTGGCAG AAGGCTGAGT TAGGCAGCAG  
73551 GGCCGGGAGC GTCTGCCCTC CACAGGGTGG GGGACAGATA GGCTAAGCGA

FIGURE 3A-32



73601 CTCCCAGCTT GCTACCCTCA GTGGCCAGTG TGGGCGTGGG CGGTTTGGGG  
73651 CGCTTGGCTG GTGGTGGCCA CTGCATCCCT TAATTTATTT CTCTGCTGTT  
73701 TCTGTTCTTG AGAAATTGGG GGTGGGAGTC CTACACAGAG GCTGCCCCTA  
73751 CCCTCACCTG AGTTGTACAT TTTTTTGTGA TGGGTTTTAT TTTTATTAT  
73801 TTTATTTTAT TTTTTTTTTT TTTTGATTTA TGATGACTCC ACCCCTCTTC  
73851 ATCACCCCCG CTCCCAGGCC AGGCTCAGCG ATTAAGCCGA GCCCTTGCGT  
73901 CCTAGGAAGG GGCCTTGCCA ACCTCAGCCC TCCTGCCCCA CACTCCTACT  
73951 GCGGCTCAGA CCAAGGGCTC CCCCTCCCTC CCTTCCCCCC TCCTGCCCTA  
74001 TGGAACAGCC CGGGTGCTCT GAGGGGGCTG GGAGGGCATG GCTTGGCTCC  
74051 CAAAGGGGGT AGGGGCCCCG GGCACCCAGG CAAGGTGGCC CCTCCCCGTC  
74101 TAGCCCCCTC CTCCCCAACC CTGCACTTAG TTTCTCCTCT GGATCAAACA  
74151 CGTAATAAAG AGAATGTTTG GAATCTGAGC TGCCTCCTCC TGTCTCTTCT  
74201 CCCAGCCAGG CAGGGACCCA GTCTCCTGTG GGCAAGATGT GGCCTAGCCC  
74251 ACCTGCCTTG CAGGAGAGAC TTGATTCTCT TCTGGGGCCA GTGCTGGGTG  
74301 GGCCCAGCTC CCCACTTACC CACAGGGCAC AGACAGGAAG CAAAGCCCAG  
74351 GGCCCTTGCA CCAAAAGGGA AAGAAAACCT AGTAAGCTTA GATTTTATTT  
74401 TTTTAAATTT TTAATAAATG TTGAAAAATA AATCCATGTC TGCATAAGTT  
74451 CCCAACCCCC ATTTCTCAA GTTTCTGGAA GGTGGGCTTG GTGGGCACCC  
74501 TCAGCTCCTT AGCATTTCCC AGCTGGCCCC TGAAGACAGA GCTTCTCTTC  
74551 CAGCCTCTGC TGCTGTAAGG CCCCTCTGCC CACCTCCCCC CCTGCAGCCT  
74601 CCCTCCCCAC CTCACCCAG ACTTATTGCT AAAAGAAGGG AAAGAGGAAT  
74651 GAGAACAGCC AGCACACCCA ACTGCCCTCT CCCCCTCCA CGCTAAGGTC  
74701 ACTACCCCGG ACACACAAAG GGCAGGACCC AGAGGCCAAG CCCCAGCAGA  
74751 CTAGGACACA GCCATTCCAG TACCGGCCAG GAAGCGAAAG TGCCCTCAGG  
74801 CCAGCTCAAA GGCCCTGAG CCCGGCCATG GCCCCAGGAG ACAGGCCAG  
74851 CTGCCAGGAA CACATGCAGA ACCCAAAGGG CGGGGCTGGG CTGTCCGAAA  
74901 CTCTGGTCTT ACAAAGACCC CGCCAGAGCC CTAGTCCCTT CTGTCTCAG  
74951 TGACACCAGA GATGCCTGGG GATGGCCAGC AAAGGGGTCC TGGAGCCCGT  
75001 GGTGTTGTTGA GGACGTCAGG GCTCAGAGTG AGGGTGCTGG GGGCTCCAGA  
75051 GGGGTTCCAA TCAGGGTGGG TGGGGGCTGA GGGCCAGGGC GGGCGCTGTG  
75101 GCGGGGGGCA GCCAGAGCGG GCGGATGAG AGGCGGTGGG GGCTGGTTGG  
75151 GGGCCAGCCG GGGCTGGAGG AAGCGGCCCT GCTGCAGTGG GGGTGGCTGT  
75201 CGGAGCAGAG TGGGAGCCGT GGGCAAAGGT GGCCTCAGCA GCGGGGTGG  
75251 CTGGGACAGC GAGGTGGGAG GTGGAGGGGG TGGTGGCGCA GGGGGCACTG  
75301 ATCGGGGCAC GGACGTGGAG ACCGATGTAA TCTGGACCTG AGGGGAGAGG  
75351 AAAGAGTGAG AAGCCAGGCT CTTCCCGCCC TCAGCCCAGT CTAAG (SEQ ID NO:3)

FEATURES:

Genewise results:

Start: 2396

Exon: 2396-2449

Exon: 58311-58490

Exon: 58732-58785

Exon: 61383-61431  
 Exon: 61759-61824  
 Exon: 61914-61988  
 Exon: 62207-62259  
 Exon: 63025-63261  
 Exon: 63710-63829  
 Exon: 63931-64030  
 Exon: 64108-64220  
 Exon: 65353-65485  
 Exon: 65759-65937  
 Exon: 66216-66313  
 Exon: 67941-68198  
 Exon: 71417-71461  
 Exon: 72034-72391  
 Stop: 72392

Sim4 results:

Exon: 2396-2449, (Transcript Position: 1-54)  
 Exon: 58311-58490, (Transcript Position: 55-234)  
 Exon: 58732-58785, (Transcript Position: 235-288)  
 Exon: 61383-61431, (Transcript Position: 289-337)  
 Exon: 61759-61824, (Transcript Position: 338-403)  
 Exon: 61914-61988, (Transcript Position: 404-478)  
 Exon: 62207-62259, (Transcript Position: 479-531)  
 Exon: 63025-63261, (Transcript Position: 532-768)  
 Exon: 63710-63829, (Transcript Position: 769-888)  
 Exon: 63931-64030, (Transcript Position: 889-988)  
 Exon: 64108-64220, (Transcript Position: 989-1101)  
 Exon: 65353-65485, (Transcript Position: 1102-1234)  
 Exon: 65759-65937, (Transcript Position: 1235-1413)  
 Exon: 66216-66313, (Transcript Position: 1414-1511)  
 Exon: 67941-68198, (Transcript Position: 1512-1769)  
 Exon: 71417-71461, (Transcript Position: 1770-1814)  
 Exon: 72034-72394, (Transcript Position: 1815-2175)

CHROMOSOME MAP POSITION:  
 chromosome 11

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
6469	A	G	Intron
10970	T	C	Intron
10977	T	C	Intron

FIGURE 3A-34

11044	T	A G C	Intron
11470	G	A	Intron
13050	T	G	Intron
13231	T	G	Intron
13813	C	G	Intron
28240	G	C	Intron
28472	G	T	Intron
36051	C	A	Intron
37118	A	G	Intron
46715	A	T	Intron
47190	G	A	Intron
50801	T	C	Intron
50877	-	A	Intron
53173	G	A	Intron
53756	G	A	Intron
55878	-	T	Intron
57192	A	C	Intron
57500	C	T	Intron
58984	C	A	Intron
59775	G	A	Intron
59869	T	G	Intron
59985	A	G	Intron
65094	G	A	Intron
73617	T	C	Intron
75055	T	A G C	Intron

Context:

DNA

Position

6469	TGGAGAAAGGTCCAGCTTCCAGAGTTCACCTGCTAGAGTTTTCCATAACACCTGGGGGAG AGGCTACTCCATCTGGGACCTGCCCCACCTCTGGGCCTCAGAACTATGAGAGAGGGATT GAGAGAAAACCTTGCCCCACTTCTGCTGCAGTGGGAAGGGAGGGGGCTGCTGTCAGGCTTC TAGGCAGTGAGCGGCATTGTTTTATTCTCTCAGTTCAGGAAGGGGAGTTTAGAAGTACTG GTGAAGAAAACAAAGTTACAAGATCCTATAAGGAACAGCTGAACTACTCCAAACACTCTC [A,G] CTGGACCCCCATTGTTGATTCTGGATAAAAATATATATATATAAACTCTTTTTTTTTT TTGACACAGAGTCTTGCTCTGTGCGCCAGGCTGGAGTGTAGCGATGCGATCTCGGCTCAC TGCAACCTCCGCCTCCCGGGTCAAGCGATTCTCCTGCCTCAGCCTCCTGGGAGTAGCTGG GACTACAGGCGCCCAACCACCATGCTGGCTAATTTTTGTATTTTATAGTAGAGACGGGGTTT TGCCATATTGGCCAAGCTGGTCTCGATCTCCTGACCTCAGGTGATCTGCTGGATAAATAT
10970	GACTCCCTTCCCAATTCAAACTTGGTGAAAGACCCTCAGCCTAGCCAGGAGGAAGGGAC TGGGTCTGCCTTTGGCTCCTCATTTATGGGTCTGGGAGGGGATCAGGACTCCTTACTGCT ATGATCTGGCTGCTAAATTCAGTGACATCCAGGCCTTTTTTCGTCCACGCAATGGGACT GTCTGTCCAGGCCTGCTGGGAAAGAAAAGAGAGAAAAAATAGTTTTTGTCTTTGGCAGC

FIGURE 3A-35

TTACAGGGACTTCAGCCATAGGAAACAACCTGTAGGAAAGGTGGGAGCTTCCGGTCACCA  
[T,C]  
GTGTGCTGACACTTCCTGCAATAGCACTAGGGAGTCTTTCTCAGGGAGCAAGGCCAGCCA  
GGTAGGATTATTTCCAGTCTCCCAGCTAAGCAGGAAATGCCAAAATATGAACGTTTAGT  
AATTAGTGAGTGTAACCTACCTGCTGACAGAGCTCCAGCCTAGACCTTGTCTTGGGGGCT  
GGTTGCCCCTGTTGATACTACAGTGAGCTACTCATTGCTTCTGATTACCATTTTCAGTATG  
AGTTTTGCTTTGGTTTCTGATATCCCATGTGCGGCTGCCTTTTTTCTCCACCTTCTTTTT

10977 TTCCCAATTCACAACCTGGTGAAAGACCCTCAGCCTAGCCAGGAGGAAGGGACTGGGTCT  
GCCTTTGGCTCCTCATTTATGGGTCTGGGAGGGGATCAGGACTCCTTACTGCTATGATCT  
GGCTGCTAAATTCAGTGACATCCCAGGCCTTTTTTCGTCCACGCAATGGGACTGTCTGTC  
CAGGCCTGCTGGGAAAGAAAAGAGAGAAAAAATAGTTTTTGCTCTTTGGCAGCTTACAGG  
GACTTCAGCCATAGGAAACAACCTGTAGGAAAGGTGGGAGCTTCCGGTCACCATGTGTGC  
[T,C]  
GACACTTCCTGCAATAGCACTAGGGAGTCTTTCTCAGGGAGCAAGGCCAGCCAGGTAGGA  
TTATTTCCAGTCTCCCAGCTAAGCAGGAAATGCCAAAATATGAACGTTTAGTAATTAGT  
GAGTGTAACCTACCTGCTGACAGAGCTCCAGCCTAGACCTTGTCTTGGGGGCTGGTTGCC  
CCTGTTGATACTACAGTGAGCTACTCATTGCTTCTGATTACCATTTTCAGTATGAGTTTTG  
CTTTGGTTTCTGATATCCCATGTGCGGCTGCCTTTTTTCTCCACCTTCTTTTTGTTGTGT

11044 GCTCCTCATTTATGGGTCTGGGAGGGGATCAGGACTCCTTACTGCTATGATCTGGCTGCT  
AAATTCAGTGACATCCCAGGCCTTTTTTCGTCCACGCAATGGGACTGTCTGTCCAGGCCT  
GCTGGGAAAGAAAAGAGAGAAAAAATAGTTTTTGCTCTTTGGCAGCTTACAGGGACTTCA  
GCCATAGGAAACAACCTGTAGGAAAGGTGGGAGCTTCCGGTCACCATGTGTGCTGACACT  
TCCTGCAATAGCACTAGGGAGTCTTTCTCAGGGAGCAAGGCCAGCCAGGTAGGATTATTT  
[T,A,G,C]  
CCAGTCTCCCAGCTAAGCAGGAAATGCCAAAATATGAACGTTTAGTAATTAGTGAGTGTA  
ACTACCTGCTGACAGAGCTCCAGCCTAGACCTTGTCTTGGGGGCTGGTTGCCCCTGTTG  
ATACTACAGTGAGCTACTCATTGCTTCTGATTACCATTTTCAGTATGAGTTTTGCTTTGGT  
TTCTGATATCCCATGTGCGGCTGCCTTTTTTCTCCACCTTCTTTTTGTTGTGTCTTTTTG  
TTTTTTTGAGACGGAGTCTTGCTCTGTTGCCAGGCTGGAGTACAGTGGCACAATCTCAG

11470 ACAGTGAGCTACTCATTGCTTCTGATTACCATTTTCAGTATGAGTTTTGCTTTGGTTTCTG  
ATATCCCATGTGCGGCTGCCTTTTTTCTCCACCTTCTTTTTGTTGTGTCTTTTTGTTTTT  
TTGAGACGGAGTCTTGCTCTGTTGCCAGGCTGGAGTACAGTGGCACAATCTCAGCTCAC  
TGCAACCTCCGCTTCCCAGGTTCAAGCAATTCTGCCTTAGCCTCCCAAGTAGCTGGTACT  
ACAGGCATGTGCCAGCACACCCGGCTAATTTTTTTTTTTTTTTTTTTTGAGACAGGGTCTC  
[G,A]  
CTCTGTGCGCCAGGCTGGAGTGCACTGGCGGATCTCAGCTCACTGCAAGCTCTGCCTCC  
CGGGTTACACCATTTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTTCAGGCGCCACCC  
ACCATGCCAGCTAATTTTTTTGTACTTTTTTTTTTTTTTAAAGTAGAGATGAGGTTTCACC  
ATGTTAGCCAGGATGGTCTCAATCTCCTGACCTCATGATCCACCCACCTCGGCCTCCCAA  
AGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCTGTAAACCTGGCTAATTTTTGT

13050 ATGGGAGAAGAATAGTACCCATCTTATAGGTATAGCTGTTATGAGTATTAAGAGTTAA  
TGAATAGAAAGCATTTAGAATAGCGCCTGGCACAGCAGAATGATCATTGTATTATTGTT

FIGURE 3A-36

CCAGTTGAACAACACAGTGAATTTTATCTGAGCACCACAACTCTAGGTCAGTATAAGG  
GGTGATGTTTGGGATTTCTCTGTAATCAGTTGAAAAAATCTTGTTCTGGCATCTTCAAGC  
CACTGGGGTCTATAGGTGCTTTTTCTAACATTTCTGTTTTTTTGTGTTGTTGTTGTT  
[T,G]  
TTTGAGATGGAGTCTTGCTCTTGTTACCCAGGCTGGAGTGCAGTAGCACCATCTTGGCTC  
ACTGTGACCTCCACCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTG  
GGATTACAGGCACCTGCCACCATACCTGGCTAATTTTTTTTTTTTTTTTTTTTTT  
TATTTTTAGTAGAGATGGGGTTTACCATGTTGACCAGGCTGGTCTTGAACCTCTGACCT  
CATGATCTGCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACC

13231 GTGATGTTTGGGATTTCTCTGTAATCAGTTGAAAAAATCTTGTTCTGGCATCTTCAAGCC  
ACTGGGGTCTATAGGTGCTTTTTCTAACATTTCTGTTTTTTTGTGTTGTTGTTGTTT  
TTTGAGATGGAGTCTTGCTCTTGTTACCCAGGCTGGAGTGCAGTAGCACCATCTTGGCTC  
ACTGTGACCTCCACCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTG  
GGATTACAGGCACCTGCCACCATACCTGGCTAATTTTTTTTTTTTTTTTTTTTTT  
[T,G]  
ATTTTTAGTAGAGATGGGGTTTACCATGTTGACCAGGCTGGTCTTGAACCTCTGACCTC  
ATGATCTGCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCC  
GCCCTAGTTTGCTTTTTTACCAATCACCTATCTGAAAAAATGGAATGCTACTGGAGAG  
ATTCATGTACTTCTGAGAACACTTTTAGCTCATTTTTTATAAGGCATCAATATTAGATAG  
TTTTCTTGATTAAAGAAAAAAAACACCACCCACTGCCTGCCTATATTTCTGGGTTGCAA

13813 CTATATTTCTGGGTTGCAAATGATGGCGGTGGATGTGCAGCCTCATCCGTGGCTAGAAGG  
CCAAATCCAAAGTCACCAGAGCTTGAGTTTTTTGAGAGTTGAGATCTGTGTGTCAAAGGG  
GAAGCCCTAGGGTGGTTCTCTGCAGCACCAGAGCAGGGATTACATACCATCATGTTCTT  
TCTTTTTCTTTCTCGTCTTTCTTTCTTCTTTCTTTTGTCTCATGATTCTCACT  
GTGTTGCCCAGGCTGGTCTTGAATATTGGCCTCAAGTGATCCTCCCGCATTGGCCTCCC  
[C,G]  
AAGTGCTGGGATTACACACTCAGCCATGTTCTTTCTTCAAGTACGGTATTGACCCTTTG  
GCCACAGGAGAACGTGCCAGTTTTCTTAAAGACCACGTGGGAACCTCAGCAGCCCATGA  
TTGTAGGTTCTTTTTCCCTCATAGAGTGGCCTTCAAGGGCAGGTTCTTGTTATCTGCGT  
TTCAGAGACCCAAAGGGACACAGGCATTTCTGCTCCTGGGAATTTGCGGACTTTGAATCT  
TGAGCTCAGATTTTGGTCTCTGTTGGTTGCTTGTTATCTTCATCTCTTGTCAATTTCTGG

28240 TATTAATAAATAAATAAGATTTACTTATCCAAAAGCACAAATTATGTGCCTTTTTCTTT  
TCTTTTGAGACGAGAGTCTGACTCTGTTGCCCAGGCTGCTGTAGTACAGTGACGCAGTCT  
C  
[G,C]  
GCCTTGACCTCCCAGGCTCAAGCAATCCTCCACCTCAGCCTCCCAAGTAGCTGGGACTA  
CAGGCATGTGCCACTATGCCTGGCTAATTTTTTGCACTTTTTGTAGAGATGGGGTTTCGT  
C

28472 TTTCTTTCTTTTGAGACGAGAGTCTGACTCTGTTGCCCAGGCTGCTGTAGTACAGTGAC  
GCAGTCTCGGCCTTGACCTCCCAGGCTCAAGCAATCCTCCACCTCAGCCTCCCAAGTAG  
CTGGGACTACAGGCATGTGCCACTATGCCTGGCTAATTTTTTGCACTTTTTGTAGAGATG  
GGGTTTCGTATGTTGCCCAGGCTGGCCTGGAACCTCTGGCGTCAAGCAACCTACCTGCC

FIGURE 3A-37

TTCGCCTCCCAGAGTGCTGGGATTACAGGCAGTCGCCATTGTATCCAGCCCAGTTATGTA  
[G,T]  
TTATGTGCCATTTCTAAACTACTTTAGAACCCATCTCTTTGGTGTGTTGTTTGTGAGAC  
AGAGTCTCACTCTGTCACCTCAGCTGGAGTGCAGTGGTGTGATCTCAGCTCACTGCAGCC  
TCGGCCCCCAAGGTTCAAGCGACCCTCCACCTCAGCCTCCCAAGTAGCTGGGACCACAG  
GTGCTCTTTTTGTAAAGAGTGGAAAAGCCAAGGTCCATGTACTTTTTTTGAGAAAGACAG  
CCTGTTGGCTTTCTTCAGAGTGGTTCTGCCCTTCCCGTACCCCATCTCCAACACATTTT

36051 CTGCCCACCTCCTGCTATGTTCTAGTTCTGATAGGAGTACCATTCAAGTTCCTTGGCAGG  
GGACCAACCCGCTTCTACCGTGGTTGGTTTCCCTCCTTTTCCCAGCTTGTTTGATGTGC  
ACGTTCTCCAAAATCTTATGCAGCTGGTTGGCTCTGTAGTGCCCAGAGATTGGAGCTCC  
TGCAACGGGAACCCCGCGCTTCCCTCCCTGGTTTTAGGGGCAGGGCTTGAAAATAAAGA  
ATCATAATCTCCCTTCTCCTCCTCCTCCTCTCCCCACTTCTCCCTGCCCCACCCCCA  
[C,A]  
CCCCACCCCAACCCTGCCAGGCAAACCTGGAGTGACCAGCTCAGAGCGGGACTCAGTCCAC  
CTCCCTGCTCTGCATGTGAGCAGTGTCTGGAGGAGATTCCGGGGCGCATGAGTATGTGA  
ACTCTGGAGCACGTTACTGTCCCGGGCTGGCACTCTGTGGCAGGTGTGTGCACTCATTCT  
GCTGTTACTGGAGACCACTCTCCTTAGGGGTGATGGTGACCCAGCTAGATGTCTGCCAGG  
TCTGTCCAAGGCCACCTGTTCTCTAATAGCTTGGGAAATGGAAAGCACTTCTAAATACC

37118 ACGGAGTCTTGCTCTGTTGCTCATGCTGGAGTGCAGTGGCGCGATCTCGGCTCGCTGCAA  
CCTCCACACCCAGATTAAAGCGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGAGACTGC  
AGGCATGCGCCACCACGCCCAGCTAATTTTTGTATTTTAAATAAGAGACAGAGCTTCACC  
ATGTTGGCCAGGCTGGTCTTGAACCTCCGAACTCAGGTGATCCGCCTGCCTCGGCCTCCC  
GAGGGACTGGGATTACAGGCATGAGCTACTGTGCCCAGCCTGAAGATTGGTTATTTAGGG  
[A,G]  
CTGTGACAAATGGTTTTGAGAGGAGCACTGGAAAGCCTGTAACCTCACAGAGCCAGGGG  
TCAGCTTTTGTGCCATAGCCTTATAGCTTCTGTGGCCTGTAGTGCCTGAGGCCAGGGGAT  
CAGGTGCTGACCACCTTTCCCTCTTCTTCTGTGTCTTGCGGCCAGCGACTGTTATTGT  
CAGGTTGACCCTCTGGTTAGAGAGGATGACTTTGGCCTGGTGTCCAGACTCCCTGCTGCC  
TTATCCCCTCTGCCCTGGAACCTGCACCTAAAAACAATTACTTTCCTCCTGATTCCAACAT

46715 CACCATGTCATTCACTACTCCTCCTGCAGGATGGTTTTATGTTAGGAAAGAGGGTCCTC  
TTTGCCTGATTGCCAGCCATGGCAGAATTTGACTTTTCTTGTATAGAGGGAATACCA  
GGATGACAGGAATCAACTTAGCTATACTGGTACTTACAGTCAAATTTCTAGGTATTGTAG  
CTCTTCCCAGAGCCCAGAGAACCTTGGAGAGGGGAAACAATGGTTCTACCCAAAAATG  
AAGCTAGATAATAATAGAATACATCATCAAGACATTACTGAACACCACGTTCTATGGTAA  
[A,T]  
CACTGACATGGATTTTCTTTTTTTTTTCTTTGAGACAGGGTCTTACTCTGTCACCCAG  
GCTGGAGTGCAGCAGTGTGATCACGGCTCACTGCAGCCTCAGCCTACCTCCCTGGGCTCA  
GGTGATCCTTCCACCTCAGCCTCCCAAGTAGCTGGGATTGCAGGCACTTGTCAACACACC  
CCGGCTAATTTTTGTGTTTTTTGTAGAGCCTGTGTTTGCCATGTTGCCAGGCTGGCC  
TCGAGTTCCTAGGCTCAAGGGATCTGCCTGTCTTGGCCTCCCAAAGTGCTGGAATCAGAG

47190 CACACCCCGGCTAATTTTTGTGTTTTTTGTAGAGCCTGTGTTTTGCCATGTTGCCAGG  
CTGGCCTCGAGTTCCTAGGCTCAAGGGATCTGCCTGTCTTGGCCTCCCAAAGTGCTGGAA

FIGURE 3A-38

TCAGAGGTGTAAGCCACCACGCCCCGGCCAGATTTTCTCATTTAATCTTCACTCTAATTCT  
GTGAAATGGGTACAGCTAGTATCTTTATGTCCCAAATGAGGAAACAGATTTGGAGAAGTT  
ATGTCACCTTTGCTCATGTTCACTCAGCTGGTAAGCAACAGAGGTGGGCAGAGCGACTATA  
[G,A]

TAAGTTTTCTGTATAGTTTACCTCTTCTAAGTTTTCTGGAAGGCAGGAGCCAGATCGCACT  
GAGCTTTGCAACTGGAGCCAGGGCTCCAGAGTACTGCTCAACAAAGGTTTGCTAGGGCAA  
CAGTAGCTGGGGATTTAGCGACCAGACCCCAGCAAGCAGATTCTCAGGGATGAAAGTAGT  
CCTGGAAGCCTCTAAAGCCCTGGTTGCTCAGTAGAATCTAGTTTCAAGAGGAGCCAGCA  
TTTCAAGTGGCTCTGAAGACAGAGGAGATTTGGAGAGTGCTCTTTGCATTGTGGCTTCCA

50801 CTCTGAATGCCAATTTCTCAATGGAAAACAGGGAGACTACCTACCCTATAGGTCTGTGTT  
TGGAGAAAACAAAGTGTAAGCGCTGGACATACAGTAGCATCAGAAATGCTGAATCCGTTG  
GCCAGGGCTCATGTGTAAGGCAAACATTTCTTGGCCACTCCTGAGTAGCATGGTCTTGCA  
GGAATATATGCTTAAGTGCTGTGAGAGCACAGAGGAAGCTTTGCCCTTCCCTAGAGGGTT  
AATGGCTACCAACGTGAGAAGGTCACGGAGTTCCTTAATGAGAGGGAGCCTAGCCTAGAA  
[T,C]

AGGGGATGAATGAGAAATTGTTCTGAGAACCAGAGGCAAGGCTGCAACCAGCACATAGAC  
AGGGGTCGTTGGTCTAGAAGGGGAGTCTTCTCCAGATGAGAGACAGCCAGCTTGCCCTGT  
GCTCACCATGTGCCCAGATAGTGGGGGCTTAGCAGGAGGAAGGTGTGAGGAATCCCAGGC  
CTTTGGAATTCCTTGAGAAAGCAGTGTTGTTTTGAAGGTAAGGCAGGGGATTGGTGACTG  
GAACTTGGAGGTGAGTGAGAACCTAGGGATGAACGTTCAGAAGCAGGGCTGGAAGGAAC

50877 TAAGCGCTGGACATACAGTAGCATCAGAAATGCTGAATCCGTTGGCCAGGGCTCATGTGT  
AAGGCAAACATTTCTTGGCCACTCCTGAGTAGCATGGTCTTGCAAGGAATATATGCTTAAG  
TGCTGTGAGAGCACAGAGGAAGCTTTGCCCTTCCCTAGAGGGTTAATGGCTACCAACGTG  
AGAAGGTCACGGAGTTCCTTAATGAGAGGGAGCCTAGCCTAGAATAGGGGATGAATGAGA  
AATTGTTCTGAGAACCAGAGGCAAGGCTGCAACCAGCACATAGACAGGGGTCGTTGGTCT  
[- ,A]

GAAGGGGAGTCTTCTCCAGATGAGAGACAGCCAGCTTGCCCTGTGCTCACCATGTGCCCA  
GATAGTGGGGGCTTAGCAGGAGGAAGGTGTGAGGAATCCCAGGCCTTTGGAATTCCTTGA  
GAAAGCAGTGTTGTTTTGAAGGTAAGGCAGGGGATTGGTGACTGGAACTTGGAGGTGAG  
TGAGAACCTAGGGATGAACGTTCAGAAGCAGGGCTGGAAGGAACTTAAAAGGGACATTTG  
GATTGTTTCTAGCTTTTGGGCAAATCTAGGATTAATATGATTTTTTTCATTGATAGAAT

53173 GCTTAGTAACACTTGGTTTGCCTTTTGGTTCCAAATAACTGCCTTGCAAGGGTGACCCCT  
TATTCTTTCTAAAGGCTACTTGAGAGCCATAGGGTCTACTCTTGACAGACCTCCTCCATC  
CTTTAGGGCCTGTCTAGAGTATGATATAGGCCAGAGCTTTGGGAGTGCCTGGTGTGCCAC  
GTCTTACTATAAGCAGGGAGGATGGTGGTAGAGGGGAGAGCGTGGCTTTTGCCAGGTCCT  
ATTGAGTTGGCCCAGCAGGGCAGCTAATCCTCAGCCTGCCATCCTGTTGGTGAGACCCAG  
[G,A]

GCCAAGCTGAATGGTGCAGCCAGAACCAAAAAAGAGAACTCTCTCTCCATATTAGCCAC  
TGCATACTCTTACCTCTTTATCCTTCAGGGAAGAAGCTAGGTGAGGAAGTTGCCTCACTT  
GGGGCCTTGCCCAAGAAGCATTTCTGTTGGAGACTCTCTCCTCTCTTTTCCCTTTTCT  
TTTCTCTGCTTCCTTCCAGTGGCTTGCCCTTACCCTGGCTCACATCCCTGCTGTGGGA  
AACATCTTACAGCATAGAAGAAGGGGTGAGGGGTAAAGTAAGGGAAGGATTGAGCACTTG

FIGURE 3A-39

53756

GGAAGGATTGAGCACTTGGAGTCCTCTGAGTTGGATGGTTCAGTCCCCGAAAAGGGGGTTG  
GTGACTTTGGAGCAGGGGATCAAAGAGCAAGCACCAGTGCTTGTGCTTCTCTGGCTCCT  
GAACAAGCAGAACCTCCTCTCTTTCCCTGTCTGGATACCCAGCGTGGGACCAGCCCTTC  
ACAGCCACCCTGTCTTGAGTTCCTGACTCTCCTCCTTCCCTCTTTGAAGGCTAGAGGTG  
CTGGTGTGCGCTAGCAACAGGTTGAGGGAGTGTGGCATTTCACCAGGTCTGGAGGAGAGC  
[G,A]  
GGCACTCAACCTGGCCCCCTTCTGCGGAAAGGCCCGTAGCATCTCTTGTGAGCCTTCAGCT  
GAGCTGTAGCTGGCTTAGCGGGCTCAACTTCGATTTGGAAGGTTGTTTTGACAGTGAGAC  
TTCTGGATTGGCAGACAGTAGTATTTGGGGACATAATGATTGCTCTTATTGAACATCGGA  
TAAGGCATTTTACATGTGCTCTTTCATCTACCTGTGTAAAGTAGGGAATGTTTATTGCCA  
CTTTACAGATAAGGAAATTAAAGCTTGACGTGGGGGAGCCAGGGCTTGAACCTGATTCT

55878

TCTAGGAATGCTGGACAGTTCCTTGGGTAGTAGCAAGTCATTCTTTTTTCTCTGTGGTT  
TTTGAGTGCTTCACGTACAGCCAGCAGGGGCCATGAAAGGAAGAACTTCACTCACACTC  
CTCTGGTCACCCTGCTGCCCTCCAGACTGTTTCTTGAAGTTTCAAGGCAGCTCTGGAT  
GGTTCTGGGATGAGGCTCTGGCCTCATATGCTTTGTTGCAGTATGCTGGAGCGATCGCTC  
CAGATGTTCTTTGTGAGATGTAAACCAGGGCGCTAATCAGGAGTTAGACCAGACTCTGCA  
[-,T]  
TTTTTTTTTTTTTTTTTGGAGACAGGGTCTCGCTCTATCACCCAGGCTGGAGTACAATGG  
CATGATCATGGCTCACTGCAGCCTCGAACTCCTCCTGGGTCAAGCGATCCTCCCGCCTC  
ATCCTCCAGAGCAGCTGGGACTATAGGTGCATGCCACCACACCCAGTTGATTTCTTAATT  
TTTTTTTTTTTTTTTTTGGAGACGGAGTTTCACTCTTGTTGCCAGGCTGGAGTGCAGT  
GGTGGCATCTCAGCTCACTGTAACTCCTCCTCCTGGGTCAAGCAATTCTCCTGCCTCA

57192

CCACAAGTGGAATTTCTACACGTAACCCCATATGACAGGTTATAAGCAAAATTCAATCA  
CTTTATTTTCATGCACAAAATTTATTTTAAATGTCATGAAATTACCTTCAGGCCATGTATA  
TAATGTACACATGAAAAATAAATGTTTAGACTTGGGTCCCATCCCTGAGATATCTGATTA  
TGTATATGCAAATATTCCAAAATCCAAAACAATTTAAATCTGCCAGTTTCTGGTCCTA  
AGCATTTTGGATAAAGGATATTCAACCCGTATTATGTTTATATGCCTCTTCAGTGCTGGT  
[A,C]  
GTTGTAGCTTCTGCTTCCTCATCCCCTCATTTGAGCCGGGTGGCAGAGCAGGGCAGACTG  
CTGCCTTGCTCAGACCTAATCGTTCAGTTCTTTCATTGTACAAGTATTCATTGAGCAGCA  
AACATAAGCCAGTCTCTCTAAGTGCTGGGATGTATCAGTGAATAAAGAATATATGCCTGC  
TTTCATGTGCTTCCATTTTACTGGGGGAGATGGCAAATAAATGTAAAGTGATAAATAAC  
AAAGGTTCAGTGGGGCATTCTAGTTCAGCGGCAGAAATTTCTGTCCTACGCGGGAGAC

57500

CTTCTGCTTCCTCATCCCCTCATTTGAGCCGGGTGGCAGAGCAGGGCAGACTGCTGCCTT  
GCTCAGACCTAATCGTTCAGTTCTTTTATTGTACAAGTATTCATTGAGCAGCAAACATAA  
GCCAGTCTCTCTAAGTGCTGGGATGTATCAGTGAATAAAGAATATATGCCTGCTTTCATG  
TGCTTCCATTTTACTGGGGGAGATGGCAAATAAATGTAAAGTGATAAATAACAAAGGT  
CAGTGGGGCATTCTAGTTCAGCGGCAGAAATTTCTGTCCTACGCGGGAGACTCGGGTT  
[C,T]  
GACTTCGGCCATGCAGTCCTTCCATGCAGGAAGGGCTACTACGTTTCTACCCAACAAAGT  
TATTATGGCTGGACGCAGTGGCTCACGCCTGTAATTCAGCACTTTGGGAGGCCAAGGCC  
GGCGGATCACCTGAGATCAGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCTATC  
TCTATTGAAAATACAAAATTAGCCAGGCGTGGTGGCGCATGACTGTAATCCAGCTACTC

FIGURE 3A-40



GGGAGGCTGAGGTGGGAGAATTGCTTGAACCCGGGAGGTGGAGGTTGCGGTGAGCTGAGA

58984 TTTGCTGGTCAGAGAAGTGATTTGGGGCCTTTTGTCTCATCCTCAGGTAGCTGTGAAG  
ATCATTGACAAGACTCAACTGAACTCCTCCAGCCTCCAGAAAGTAAGCACATGGCACCTC  
CTGTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGAGTCAGAGCCTCACTCTTGTGCCCC  
AGGCTGGAGTGCAATGGTGTGATCTCGGCTCACTGCAACCTCCGCCTTTTGGTTTCAAGC  
GATTCTCCCGCCTCAGCCTCCCGAGTAGCTGGGATTATAGGCACCCGCCACACACCTGG  
[C,A]  
TAAGTTTTGTATTTTAGTAGAGATGGGGTTTACCATGGTAGCCAGGCTGGTCTCGAAC  
TCCTGACCTCAAGTGATCCGCTCGCCTCGGCCTCCCAAAGTGCTAGGATTATAGGCGTGA  
ACCACTGCCCCCAGCCACCTGTCCCTTTCTAAATCTCTCTTCTGGGGTCAATGATCTAC  
TGACCCCATTTAGACCTTCTCTTGAATTCCTAGTTTAAATTTTCTGGCCATTTGCTCAC  
CGTCCCCCAACCATTCCCTCCCATGGCTCTGCTACCTTCGGGGCTTTGGTTGGATCATCT

59775 AGATCTGGAATGATACAGGGGAGTGGCTTTAGAAATACAAGAATAAGAGGAAGCAGGGAA  
CCTGCCGGTGGGTTCTGTGCCAGCTACCTTTAGAGAATGAGCTCCAGCTCAAATTTTCT  
GAACAAAACCTAGTTCTGTTTCATCTTGTGGCAAATCAGATATTTTCTCCATAAGCATATT  
GTGGCAGTTGAGTTAGGAGAAGGCATGATTCTGTGCTAACAGAGTCAGATAGTGATACTGG  
GAACCTTAGGAGTAAGGGCTGAGGATTGTTGTTGAGGGCGATGCTCATGGAATTAGAGTG  
[G,A]  
ATGAGTTGTTCTCCGGACATGCAAATAGCCAGAACCAAGGTGTTTCCTATTTATTGTTAC  
CCCTGGGATCCCTTCAAGGGTCTTTCAGTTTCAGTAGAAACATTGTTGTCATCATCAGGGT  
GTCTCTGCTTGAAGCTTTCCAGGAGGAAGGGAAAAAGGGCTGCTTATGACATCCTGGCTC  
CAGCCCCACAGAAGAAGTCAGCGTGGGGTAGGCCATTTGGCCTTGGGAGCAGTCTAGCCT  
GCCATCGTAATAATCGCCAGTCCACCAAGCCATCTTATTCCTGACCTTGTTTTCTCCCT

59869 AGAATGAGCTCCAGCTCAAATTTTCTGAACAAAACCTAGTTCTGTTTCATCTTGTGGCAA  
TCAGATATTTTCTCCATAAGCATATTGTGGCAGTTGAGTTAGGAGAAGGCATGATTCTGTG  
CTAACAGAGTCAGATAGTGATACTGGGAACCTTAGGAGTAAGGGCTGAGGATTGTTGTTG  
AGGGCGATGCTCATGGAATTAGAGTGGATGAGTTGTTCTCCGGACATGCAAATAGCCAGA  
ACCAAGGTGTTTCCTATTTATTGTTACCCCTGGGATCCCTTCAAGGGTCTTTCAGTTTCAG  
[T,G]  
AGAAACATTGTTGTCATCATCAGGGTGTCTCTGCTTGAAGCTTTCCAGGAGGAAGGGAAA  
AAGGGCTGCTTATGACATCCTGGCTCCAGCCCCACAGAAGAAGTCAGCGTGGGGTAGGCC  
ATTTGGCCTTGGGAGCAGTCTAGCCTGCCATCGTAATAATCGCCAGTCCACCAAGCCATC  
TTATTCCTGACCTTGTTTTCTCCCTAATTCTTCTTGGTTTTCTCCCTAATTCTTCTGA  
CTCTCTGGAAGGCACCAACACCAGACAAATAGAGCCATTTTCAAACCTTTGAGACTCT

59985 CGTGCTAACAGAGTCAGATAGTGATACTGGGAACCTTAGGAGTAAGGGCTGAGGATTGTT  
GTTGAGGGCGATGCTCATGGAATTAGAGTGGATGAGTTGTTCTCCGGACATGCAAATAGC  
CAGAACCAAGGTGTTTCCTATTTATTGTTACCCCTGGGATCCCTTCAAGGGTCTTTCAGT  
TCAGTAGAAACATTGTTGTCATCATCAGGGTGTCTCTGCTTGAAGCTTTCCAGGAGGAAG  
GGAAAAAGGGCTGCTTATGACATCCTGGCTCCAGCCCCACAGAAGAAGTCAGCGTGGGGT  
[A,G]  
GGCCATTTGGCCTTGGGAGCAGTCTAGCCTGCCATCGTAATAATCGCCAGTCCACCAAGC  
CATCTTATTCCTGACCTTGTTTTCTCCCTAATTCTTCTTGGTTTTCTCCCTAATTCTTC

FIGURE 3A-41

CTGACTCTCTGGAAGGCACCAACACCAGACAAATAGAGCCATTTTCAAAACCTTTTGAGA  
CTCTTTGTTACTAAAGCCAGTCTGATTCTGGCCAAAAATGTGATCTCAGCAATGATCCCT  
GAAAAATGAACATTGAAGAAGCTAGCCCCCTCAGGGGTCTAGACAAGCCCAGAAAACCCC

65094

CGGCTATTGAGTCTGTTGCTTCTGTCTAGTGCTTTATGTTTGGGTGTGTGATCTGTGTG  
TGTGTGTGTGTGTGTGTGTGTGTGTATGTGTCCGCTTCCCCTGTGTGGATCTGGAGACT  
TTGTGATTGTTCTTCTGCCCATTTGGGTTTTGTTTCATCATCTGAGTATCCCCACATGAAC  
TCCCAGCCTCCCTGCCCTGCTCTCCCTCTGGTGGTGGGATCCTTAAGAGGCACCTGGTGA  
CACTTGGTATAGGCCCATATTGCTCTGTGTTGAGGGGAGTGGACTTGAGTCTGGACATGT  
[G,A]

TTCTTGCGGATGTTTGTGTCTCTGGGTGTGTGGGCTTATGTATTCTTTCTGAGACTGTG  
TTTGTCA GTGTCTGTGTCA GAGCATGTGTGTCTCCAGGGTCTCTCCAGGGGGGATGTAT  
TGGTCTTACAAGTGGATGTCCGGTATGATCCTGGGGTGTTTGAGTGTTGGGAGAGGGCGG  
TATGTGTAAATGTGTCCATCCATAGGGATCTCCACATGACTTCTGCCCTCCCTTGAAGCT  
GTTTTCTGTTTCTTTCAGCTGGAAGGCGACACCATCACCCTGAAACCCCGGCCCTTCAGCT

73617

ACTGGGCACTCTGTGATGGGGGAGCCTTTGTCTGAAAGCACAGCCCTCGCCCTTCCTC  
TCCCCATGGCTTCCCCTTCATTGGCATTAACTCTGGGCACCAGCTCTCTCCATAGCAGTGA  
CTTCCCTCACCCTCTCATCTCTCAGCCTTGCCCTTTCTTCCTGACACTGTGCCCCCTC  
CTCTCAGGAGACACTGCCGAGGGCCACCTGGCAGAAGGCTGAGTTAGGCAGCAGGGCCGG  
GAGCGTCTGCCCTCCACAGGGTGGGGGACAGATAGGCTAAGCGACTCCAGCTTGCTACC  
[T,C]

TCAGTGGCCAGTGTGGGCGTGGGCGGTTTGGGGCGCTTGGCTGGTGGTGGCCACTGCATC  
CCTTAATTTATTTCTCTGCTGTTTCTGTTCTTGAGAAATTGGGGGTGGGAGTCCTACACA  
GAGGCTGCCCCACCTCACCTGAGTTGTACATTTTTTTGTGATGGGTTTTATTTTTTAT  
TATTTTATTTTATTTTTTTTTTTTTTTGATTTATGATGACTCCACCCCTCTTCATCACCC  
CCGCTCCCAGGCCAGGCTCAGCGATTAAGCCGAGCCCTTGCCTCCTAGGAAGGGGCGCTTG

75055

GACACAGCCATTCCAGTACCGGCCAGGAAGCGAAAGTGCCCTCAGGCCAGCTCAAAGGCC  
CCTGAGCCC GGCCATGGCCCCAGGAGACAGGCCAGCTGCCAGGAACACATGCAGAACCC  
AAAGGGCGGGGCTGGGCTGTCCGAACTCTGGTCTTACAAAGACCCCGCCAGAGCCCTAG  
TCCCTTCTGTCTCAGTGACACCAGAGATGCCTGGGGATGGCCAGCAAAGGGGTCTTGGA  
GCCCCGTGTTGGTGGAGGACGTCAAGGCTCAGAGTGAGGGTGCTGGGGGCTCCAGAGGGG  
[T,A,G,C]

TCCAATCAGGGTGGGTGGGGGCTGAGGGCCAGGGCGGGCGCTGTGGCGGGGGGCAGCCAG  
AGCGGGGCGGATGAGAGGCGGTGGGGGCTGTTGGGGGCCAGCCGGGGCTGGAGGAAGCG  
GCCCTGCTGCAGTGGGGTGGCTGTGCGAGCAGAGTGGGAGCCGTGGGCAAAGGTGGCCT  
CAGCAGCGGGGGTGGCTGGGACAGCGAGGTGGGAGGTGGAGGGGTGGTGGCGCAGGGGG  
CACTGATCGGGGCACGGACGTGGAGACCGATGTAATCTGGACCTGAGGGGAGAGGAAAGA